SEQUENCE LISTING

<110> Duvick, Jonathan P.
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Rao, Aragula Gururaj
Crasta, Oswald R.
Folkerts, Otto

<120> Amino Polyol Amine Oxidase Polynucleotides and Related Polypeptides and Methods of Use

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<141> 2000-09-[illegible]

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<151> 1999-07-[illegible]9

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attgtcgatc gacgtcgatg ctggtatctc tggcaaatga gatggggtca cagctcgatt 180

ggaggacgcc cgagaagcct tgttcgcgcc accacggctt gtcccatacg aagactatct 240

tgctatagna gcccaggata gaattttccg ccaatgcttg cttctgggcg ggaagaggtg 300

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Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu
            20                  25                  30

gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt     144
Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
        35                  40                  45

ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac     192
Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
    50                  55                  60

agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag     240
Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
65                  70                  75                  80

ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac     288
Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
                85                  90                  95

ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag     336
Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
            100                 105                 110

gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc     384
Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile
        115                 120                 125

gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg     432
Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg
    130                 135                 140

ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg     480
Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu
145                 150                 155                 160

cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt     528
Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly
                165                 170                 175

gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag     576
Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys
            180                 185                 190

agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg     624
Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly
        195                 200                 205

cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc atg     672
Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met
    210                 215                 220

tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct     720
Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala
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gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc     768
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Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu
              260                 265                 270

tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca      864
Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala
          275                 280                 285

ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta      912
Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val
      290                 295                 300

tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa      960
Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln
  305                 310                 315                 320

tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc     1008
Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val
                  325                 330                 335

gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cgg     1056
Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg
              340                 345                 350

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Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp
          355                 360                 365

caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg     1152
Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro
      370                 375                 380

gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga     1200
Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly
  385                 390                 395                 400

gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg     1248
Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser
                  405                 410                 415

gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg     1296
Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr
              420                 425                 430

tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa     1344
Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln
          435                 440                 445

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35 40 45

Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
50 55 60

Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
65 70 75 80

Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
85 90 95

Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
100 105 110

Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile
115 120 125

Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg
130 135 140

Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu
145 150 155 160

Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly
165 170 175

Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys
180 185 190

Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly
195 200 205

Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met
210 215 220

Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala
225 230 235 240

Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly
245 250 255

Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu
260 265 270

Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala
275 280 285

Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val
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Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln
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Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val
325 330 335

Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg
340 345 350

Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp
355 360 365

Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro
370 375 380

Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly
385 390 395 400

Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser
405 410 415

Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr
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gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt      96
Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu
            20                  25                  30

gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt     144
Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
        35                  40                  45

ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac     192
Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
    50                  55                  60

agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag     240
Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
65                  70                  75                  80

ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac     288
Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
                85                  90                  95

ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag     336
Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
            100                 105                 110
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gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc      384
Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile
        115                 120                 125

gaa gag cat agc ctt caa gac ctc aag gcc agc cct cag gcg aag cgg      432
Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg
    130                 135                 140

ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg      480
Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu
145                 150                 155                 160

cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt      528
Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly
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gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag      576
Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys
            180                 185                 190

agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg      624
Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly
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cag tat gtg cga tgc aaa acg ggtgcgtgtg gtgtcgtctc aggtgggaga        672
Gln Tyr Val Arg Cys Lys Thr
    210                 215

ctcgtttctc agtggtcatt cca ggt atg cag tcg att tgc cat gcc atg tca    720
                        Gly Met Gln Ser Ile Cys His Ala Met Ser
                                220                 225

aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa      768
Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu
                230                 235                 240

att gag cag tcg gca tcc ggc tgt acg gta cga tcg gcc tcg ggc gcc      816
Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala
            245                 250                 255

gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg tat      864
Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr
        260                 265                 270

ccc acc ttg acg ttt tca cca cct ctt ccc gcc gag aag caa gca ttg      912
Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu
    275                 280                 285

gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg      960
Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp
290                 295                 300                 305

gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg     1008
Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser
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agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat     1056
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Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp
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cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cgg aag      1112
Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys
        340                 345                 350

tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac caa      1160
Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln
    355                 360                 365

ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc      1208
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370                 375                 380                 385

aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga gct      1256
Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala
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ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg gcg      1304
Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala
            405                 410                 415

ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg tct      1352
Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser
        420                 425                 430

tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa cga      1400
Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg
    435                 440                 445

ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag              1442
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450                 455                 460
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            20                  25                  30

Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
        35                  40                  45

Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
    50                  55                  60
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Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
65 70 75 80

Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
85 90 95

Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
100 105 110

Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile
115 120 125

Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg
130 135 140

Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu
145 150 155 160

Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly
165 170 175

Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys
180 185 190

Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly
195 200 205

Gln Tyr Val Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met
210 215 220

Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala
225 230 235 240

Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly
245 250 255

Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu
260 265 270

Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala
275 280 285

Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val
290 295 300

Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln
305 310 315 320

Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val
325 330 335

Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg
340 345 350

Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp
355 360 365

Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro
370 375 380

Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly
385 390 395 400

Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser
405 410 415

Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr
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Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln
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Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
35 40 45

Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
50 55 60

Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
65 70 75 80

Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
85 90 95

Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
100 105 110

Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile
115 120 125

Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg
130 135 140

Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu
145 150 155 160

Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly
165 170 175

Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys
180 185 190

Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly
195 200 205

Gln Tyr Val Arg Cys Lys Thr Gly Ala Cys Gly Val Val Ser Gly Gly
210 215 220

Gly Leu Val Ser Gln Trp Ser Phe Gln Val Cys Ser Arg Phe Ala Met
225 230 235 240

Pro Cys Gln Arg Asn Leu Phe Gln Ala Gln Cys Thr Ser Thr Pro Pro
245 250 255

Ser Leu Lys Leu Ser Ser Arg His Pro Ala Val Gln Tyr Asp Arg Pro
260 265 270

Arg Ala Pro Cys Ser Glu Ala Lys Arg Trp Trp Phe Arg Tyr Arg Gln
275 280 285

Pro Cys Ile Pro Pro His Phe His His Leu Phe Pro Pro Arg Ser Lys
290 295 300

His Trp Arg Lys Ile Leu Ser Trp Ala Thr Ile Ala Arg Ser Ser Tyr
305 310 315 320

Gly Thr Ser Arg Gly Gly Ala Asn Lys Ala Ser Arg Ala Ser Ser Asn
325 330 335

Arg Ala Val Thr Pro Ser His Leu Pro Glu Ile Pro Ala Ser Thr Ser
340 345 350

Ile Asp Asn Gly Pro Leu Pro Val Ser Trp Ser Glu Thr Arg Asp Gly
355 360 365

Ser Gly Pro Asn Ser Pro Ser Arg Tyr Asp Lys Ser Leu Ser Gly Thr
370 375 380

Asn Ser Ala Gln Pro Thr Arg Thr Pro Gly Pro Lys Ser Gln Ser Arg
385 390 395 400

Pro Thr Cys Ser Lys Ser Ser Gly Arg Ser Ser Ser Ile Ser Lys Glu
405 410 415

Leu Arg Ala Pro Ser Met Gly Thr Ile Ser Ser His Trp Val Arg Arg
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1               5                  10                  15

ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt        96
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val
            20                  25                  30

ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg       144
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
        35                  40                  45

ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat       192
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
    50                  55                  60

gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg       240
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
65                  70                  75                  80

gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa       288
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
                85                  90                  95

gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag       336
Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
            100                 105                 110

gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg       384
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu
        115                 120                 125

atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag       432
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
    130                 135                 140

cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac       480
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
145                 150                 155                 160

ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc       528
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu
                165                 170                 175
```

```
ggt gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc      576
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile
            180                 185                 190

aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc      624
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly
        195                 200                 205

ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc      672
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala
    210                 215                 220

atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc      720
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val
225                 230                 235                 240

gct gaa att gag cag tgg gca tcc ggc tgt aca gta cga tcg gcc tcg      768
Ala Glu Ile Glu Gln Trp Ala Ser Gly Cys Thr Val Arg Ser Ala Ser
                245                 250                 255

ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc      816
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr
            260                 265                 270

ttg tat ccc acc ttg aca ttt tca cca cct att ccc gcc gag aag caa      864
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
        275                 280                 285

gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc      912
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
    290                 295                 300

gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg gtc gtc ctc      960
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
305                 310                 315                 320

caa tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac     1008
Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
                325                 330                 335

gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga     1056
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
            340                 345                 350

cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg     1104
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
        355                 360                 365

gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag     1152
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
    370                 375                 380

ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa     1200
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
385                 390                 395                 400
```

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gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt      1248
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
                405                 410                 415

tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag      1296
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
            420                 425                 430

acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt      1344
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
        435                 440                 445

caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag      1392
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
    450                 455                 460
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<210> 11
<211> 463
<212> PRT
<213> Exophiala spinifera

<220>
<221> misc_feature
<222> (1)..(3)
<223> Extra lysine in K:trAPAO

<400> 11

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Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
1               5                   10                  15

Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val
            20                  25                  30

Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
        35                  40                  45

Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
    50                  55                  60

Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
65                  70                  75                  80

Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
                85                  90                  95

Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
            100                 105                 110
```

Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu
115 120 125

Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
130 135 140

Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
145 150 155 160

Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu
165 170 175

Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile
180 185 190

Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly
195 200 205

Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala
210 215 220

Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val
225 230 235 240

Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser
245 250 255

Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr
260 265 270

Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
275 280 285

Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
290 295 300

Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
305 310 315 320

Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
325 330 335

Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly

340 345 350

Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
355 360 365

Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
370 375 380

Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
385 390 395 400

Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
405 410 415

Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
420 425 430

Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
435 440 445

Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
450 455 460

<210> 12
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer for cloning into vectors N23256 (Exophiala spinifera)

<400> 12
ggggaattca aagacaacgt tgcggacgtg gtag 34

<210> 13
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer for cloning into vectors N23256 (Exophiala spinifera)

<400> 13
ggggcggccg cctatgctgc tggcaccagg ctag 34

<210> 14
<211> 29

<213> DNA
<213> Artificial Sequence

<220>
<223> Designed oligo for 3' RACE, N21965 (Exophiala spinifera)

<400> 13
ggttcgtcgt acggacaacc ttgtatccc 29

<210> 14
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligo for 5' RACE, N21969 (Exophiala spinifera)

<400> 14
aagtggtccc cagacagact tttgtcgt 28

<210> 15
<211> 1673
<212> DNA
<213> Exophiala spinifera

<220>
<221> sig_peptide
<222> (1)..(267)
<223> yeast alpha mating factor secretion signal

<220>
<221> CDS
<222> (1)..(1662)
<223>

<400> 15
atg aga ttt cct tca att ttt act gct gtt tta ttc gca gca tcc tcc 48
Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
1 5 10 15

gca tta gct gct cca gtc aac act aca aca gaa gat gaa acg gca caa 96
Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln
20 25 30

att ccg gct gaa gct gtc atc ggt tac tca gat tta gaa ggg gat ttc 144
Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
35 40 45

gat gtt gct gtt ttg cca ttt tcc aac agc aca aat aac ggg tta ttg 192
Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu
50 55 60

ttt ata aat act act att gcc agc att gct gct aaa gaa gaa ggg gta 240
Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val

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65                  70                  75                  80

tct ctc gag aaa aga gag gct gaa gct gaa ttc aaa gac aac gtt gcg      288
Ser Leu Glu Lys Arg Glu Ala Glu Ala Glu Phe Lys Asp Asn Val Ala
                85                  90                  95

gac gtg gta gtg gtg ggc gct ggc ttg agc ggt ttg gaa acg gca cgc      336
Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg
            100                 105                 110

aaa gtc cag gcc gcc ggt ctg tct tgc ctc gtt ctt gag gcg atg gat      384
Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp
        115                 120                 125

cgt gta ggg gga aag act ctg agt gta caa tcg ggt ccc ggc agg acg      432
Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr
    130                 135                 140

act atc aac gac ctc ggc gct gca tgg atc aat gac agc aac caa agc      480
Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser
145                 150                 155                 160

gaa gta tcc aga ttg ttt gaa agt ttt cat ttg ctg ggc gag ctc cag      528
Glu Val Ser Arg Leu Phe Glu Ser Phe His Leu Leu Gly Glu Leu Gln
                165                 170                 175

agg acg act gga aat tca atc cat caa gca caa gac ggt aca acc act      576
Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr
            180                 185                 190

aca gct cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca      624
Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala
        195                 200                 205

ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc      672
Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser
    210                 215                 220

ctt caa gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg      720
Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val
225                 230                 235                 240

agc ttc gcg cac tac tgt gag aaa gaa cta aac ttg cct gct gtt ctc      768
Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu
                245                 250                 255

ggc gta gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac      816
Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His
            260                 265                 270

gag atc agc atg ctt ttt ctc acc gac tac atc aag agt gca acc ggt      864
Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly
        275                 280                 285

ctc agt aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga      912
Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg
    290                 295                 300
```

```
tgc aaa aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt      960
Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu
305                 310                 315                 320

gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag     1008
Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln
                325                 330                 335

tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga     1056
Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg
            340                 345                 350

agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg     1104
Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu
        355                 360                 365

aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat     1152
Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn
    370                 375                 380

tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg     1200
Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro
385                 390                 395                 400

tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac     1248
Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp
                405                 410                 415

ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg     1296
Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp
            420                 425                 430

tcc att acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa     1344
Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln
        435                 440                 445

cag tcc aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca     1392
Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala
    450                 455                 460

gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc     1440
Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu
465                 470                 475                 480

gaa atc gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc     1488
Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala
                485                 490                 495

gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg     1536
Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr
            500                 505                 510

ccg ttc aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg     1584
Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp
        515                 520                 525
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aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca      1632
Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala
    530                 535                 540

gaa gtt gtg gct agc ctg gtg cca gca gca taggcggccg c               1673
Glu Val Val Ala Ser Leu Val Pro Ala Ala
545                 550
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<210> 17
<211> 554
<212> PRT
<213> Exophiala spinifera

<400> 17

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Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
1               5                   10                  15

Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln
            20                  25                  30

Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
        35                  40                  45

Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu
    50                  55                  60

Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
65                  70                  75                  80

Ser Leu Glu Lys Arg Glu Ala Glu Ala Glu Phe Lys Asp Asn Val Ala
                85                  90                  95

Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg
            100                 105                 110

Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp
        115                 120                 125

Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr
    130                 135                 140

Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser
145                 150                 155                 160

Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln
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165 170 175

Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr
180 185 190

Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala
195 200 205

Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser
210 215 220

Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val
225 230 235 240

Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu
245 250 255

Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His
260 265 270

Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly
275 280 285

Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg
290 295 300

Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu
305 310 315 320

Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln
325 330 335

Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg
340 345 350

Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu
355 360 365

Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn
370 375 380

Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro
385 390 395 400

Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp
405 410 415

Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp
420 425 430

Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln
435 440 445

Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala
450 455 460

Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu
465 470 475 480

Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala
485 490 495

Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr
500 505 510

Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp
515 520 525

Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala
530 535 540

Glu Val Val Ala Ser Leu Val Pro Ala Ala
545 550

<210> 18
<211> 2079
<212> DNA
<213> Unknown

<220>
<223> GST:K:trAPAO 2079 for bacterial expression (Exophiala spinifera)

<220>
<221> CDS
<222> (1)..(2076)
<223>

<220>
<221> misc_feature

<220>
<221> misc_feature
<222> (1)..(687)
<223> gst fusion + polylinker

<220>
<221> misc_feature
<222> (688)..(2076)
<223> K:trAPAO

<220>
<221> misc_feature
<222> (688)..(690)
<223> Extra lysine

<400> 18

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atg tcc cct ata cta ggt tat tgg aaa att aag ggc ctt gtg caa ccc       48
Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1               5                  10                  15

act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg       96
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
            20                  25                  30

tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg      144
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
        35                  40                  45

ggt ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa      192
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
    50                  55                  60

tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac      240
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65                  70                  75                  80

atg ttg ggt ggt tgt cca aaa gag cgt gca gag att tca atg ctt gaa      288
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
                85                  90                  95

gga gcg gtt ttg gat att aga tac ggt gtt tcg aga att gca tat agt      336
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
            100                 105                 110

aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa      384
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
        115                 120                 125

atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa aca tat tta aat      432
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
    130                 135                 140

ggt gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat      480
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145                 150                 155                 160
```

```
gtt gtt tta tac atg gac cca atg tgc ctg gat gcg ttc cca aaa tta      528
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
                165                 170                 175

gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa att gat aag tac      576
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
            180                 185                 190

ttg aaa tcc agc aag tat ata gca tgg cct ttg cag ggc tgg caa gcc      624
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
        195                 200                 205

acg ttt ggt ggt ggc gac cat cct cca aaa tcg gat ctg gtt ccg cgt      672
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
    210                 215                 220

gga tcc ccg gaa ttc aaa gac aac gtt gcg gac gtg gta gtg gtg ggc      720
Gly Ser Pro Glu Phe Lys Asp Asn Val Ala Asp Val Val Val Val Gly
225                 230                 235                 240

gct ggc ttg agc ggt ttg gag act gca cgt aaa gtc cag gcc gcc ggt      768
Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly
                245                 250                 255

ctg tcc tgc ctc gtt ctt gag gct atg gat cgt gta ggg gga aag act      816
Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr
            260                 265                 270

ctg agc gta caa tcg ggt ccc ggc agg acg act atc aac gac ctc ggc      864
Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly
        275                 280                 285

gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc aga ttg ttt      912
Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe
    290                 295                 300

gaa aga ttt cat ttg gag ggc gag ctc cag agg acg act gga aat tca      960
Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser
305                 310                 315                 320

atc cat caa gca caa gac ggt aca acc act aca gct cct tat ggt gac     1008
Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp
                325                 330                 335

tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg gaa ctc ctc ccc     1056
Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro
            340                 345                 350

gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac ctc aag gcg     1104
Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala
        355                 360                 365

agc cct cag gcg aag cgg ctc gac agt gtg agc ttc gcg cac tac tgt     1152
Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys
    370                 375                 380

gag aag gaa cta aac ttg cct gct gtt ctc ggc gta gca aac cag atc     1200
```

```
Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile
385                 390                 395                 400

aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc agc atg ctt ttt      1248
Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu Phe
                405                 410                 415

ctc acc gac tac atc aag agt gcc acc ggt ctc agt aat att ttc tcg      1296
Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser
            420                 425                 430

gac aag aaa gac ggc ggg cag tat atg cga tgc aaa aca ggt atg cag      1344
Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln
        435                 440                 445

tcg att tgc cat gcc atg tca aag gaa ctt gtt cca ggc tca gtg cac      1392
Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His
    450                 455                 460

ctc aac acc ccc gtc gct gaa att gag cag tcg gca tcc ggc tgt aca      1440
Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr
465                 470                 475                 480

gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt      1488
Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val Val
                485                 490                 495

tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt tca cca cct ctt      1536
Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu
            500                 505                 510

ccc gcc gag aag caa gca ttg gcg gaa aat tct atc ctg ggc tac tat      1584
Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr
        515                 520                 525

agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc gaa caa ggc      1632
Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly
    530                 535                 540

ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc tca ttt gcc aga      1680
Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg
545                 550                 555                 560

gat acc agc atc gac gtc gat cga caa tgg tcc att acc tgt ttc atg      1728
Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met
                565                 570                 575

gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc aag cag gta cga      1776
Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg
            580                 585                 590

caa aag tct gtc tgg gac caa ctc cgc gca gcc tac gag aac gcc ggg      1824
Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly
        595                 600                 605

gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc gag tgg tcg aag      1872
Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys
```

```
    610                 615                 620

cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg ctg aac gat      1920
Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp
625                 630                 635                 640

ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc aag agt gtt cat      1968
Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His
                645                 650                 655

ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat atg gaa ggg      2016
Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly
            660                 665                 670

gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt gtg gct agc ctg      2064
Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu
        675                 680                 685

gtg cca gca gca tag                                                 2079
Val Pro Ala Ala
    690
```

<210> 19
<211> 692
<212> PRT
<213> Unknown

<220>
<223> GST:K:trAPAO 2079 for bacterial expression (Exophiala spinifera)

<220>
<221> misc_feature
<222> (1)..(687)
<223> gst fusion + polylinker

<220>
<221> misc_feature
<222> (688)..(2076)
<223> K:trAPAO

<220>
<221> misc_feature
<222> (688)..(690)
<223> Extra lysine

<400> 19

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Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1               5                   10                  15

Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
            20                  25                  30

Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
```

35 40 45

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
50 55 60

Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65 70 75 80

Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
85 90 95

Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
100 105 110

Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
115 120 125

Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
130 135 140

Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145 150 155 160

Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
165 170 175

Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
180 185 190

Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
195 200 205

Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
210 215 220

Gly Ser Pro Glu Phe Lys Asp Asn Val Ala Asp Val Val Val Val Gly
225 230 235 240

Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly
245 250 255

Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr
260 265 270

Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly
275 280 285

Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe
290 295 300

Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser
305 310 315 320

Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp
325 330 335

Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro
340 345 350

Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala
355 360 365

Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys
370 375 380

Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile
385 390 395 400

Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu Phe
405 410 415

Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser
420 425 430

Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln
435 440 445

Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His
450 455 460

Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr
465 470 475 480

Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val Val
485 490 495

Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu
500 505 510

Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr
515 520 525

Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly
530 535 540

Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg
545 550 555 560

Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met
565 570 575

Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg
580 585 590

Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly
595 600 605

Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys
610 615 620

Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp
625 630 635 640

Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His
645 650 655

Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly
660 665 670

Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu
675 680 685

Val Pro Ala Ala
690

<210> 20
<211> 1464
<212> DNA
<213> Unknown

<220>
<223> F:trAPAO fusion with barley alpha amylase (Exophiala spinifera)

<220>
<221> sig_peptide
<222> (1)..(72)
<223> Barley alpha amylase signal sequence

<220>
<221> misc_feature
<222> (73)..(1464)
<223> F:trAPAO cDNA

<220>
<221> CDS
<222> (1)..(1461)

<220>
<221> misc_feature
<222> (73)..(75)
<223> Added lysine residue

<400> 20
atg gcc aac aag cac ctg agc ctc tcc ctc ttc ctc gtg ctc ctc ggc 48
Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly
1 5 10 15

ctc tcc gcc tcc ctc gcc agc ggc aaa gac aac gtt gcg gac gtg gta 96
Leu Ser Ala Ser Leu Ala Ser Gly Lys Asp Asn Val Ala Asp Val Val
20 25 30

gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc cag 144
Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln
35 40 45

gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta ggg 192
Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly
50 55 60

gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg act atc aac 240
Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn
65 70 75 80

gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc 288
Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser
85 90 95

aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg act 336
Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr
100 105 110

gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct cct 384

```
Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro
        115                 120                 125

tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg gaa      432
Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu
    130                 135                 140

ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac      480
Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp
145                 150                 155                 160

ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc gcg      528
Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala
                165                 170                 175

cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta gca      576
His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala
            180                 185                 190

aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc agc      624
Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser
        195                 200                 205

atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt aat      672
Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn
    210                 215                 220

att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa aca      720
Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr
225                 230                 235                 240

ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca ggc      768
Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly
                245                 250                 255

tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca tcc      816
Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser
            260                 265                 270

ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa aag      864
Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys
        275                 280                 285

gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt tca      912
Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser
    290                 295                 300

cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc ctg      960
Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu
305                 310                 315                 320

ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc     1008
Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg
                325                 330                 335

gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc tca     1056
Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser
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                340                 345                 350

ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att acc      1104
Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr
        355                 360                 365

tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc aag      1152
Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys
    370                 375                 380

cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac gag      1200
Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu
385                 390                 395                 400

aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc gag      1248
Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu
                405                 410                 415

tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg      1296
Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly
            420                 425                 430

ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc aag      1344
Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys
        435                 440                 445

agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat      1392
Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr
    450                 455                 460

atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt gtg      1440
Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val
465                 470                 475                 480

gct agc ctg gtg cca gca gca tag                                     1464
Ala Ser Leu Val Pro Ala Ala
                485
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<210> 21
<211> 487
<212> PRT
<213> Unknown

<220>
<223> K:trAPA0 fusion with barley alpha amylase (Exophiala spinifera)

<220>
<221> misc_feature
<222> (73)..(1464)
<223> K:trAPA0 cDNA

<220>
<221> misc_feature
<222> (73)..(75)
<223> Added lysine residue

<400> 21

Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly
1 5 10 15

Leu Ser Ala Ser Leu Ala Ser Gly Lys Asp Asn Val Ala Asp Val Val
20 25 30

Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln
35 40 45

Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly
50 55 60

Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn
65 70 75 80

Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser
85 90 95

Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr
100 105 110

Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro
115 120 125

Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu
130 135 140

Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp
145 150 155 160

Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala
165 170 175

His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala
180 185 190

Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser
195 200 205

Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn
210 215 220

Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr
225 230 235 240

Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly
245 250 255

Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser
260 265 270

Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys
275 280 285

Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser
290 295 300

Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu
305 310 315 320

Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg
325 330 335

Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser
340 345 350

Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr
355 360 365

Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys
370 375 380

Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu
385 390 395 400

Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu
405 410 415

Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly
420 425 430

Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys
435 440 445

```
Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr
     450                 455                 460

Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val
465                 470                 475                 480

Ala Ser Leu Val Pro Ala Ala
                485

<210> 22
<211> 1803
<212> DNA
<213> Exophiala spinifera

<220>
<221> CDS
<222> (1)..(1800)
<223>

<400> 22
atg gca ctt gca ccg agc tac atc aat ccc cca aac gtc gcc tcc cca      48
Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro
1               5                  10                  15

gca ggg tat tct cac gtc ggc gta ggc cca gac gga ggg agg tat gtg      96
Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val
            20                  25                  30

aca ata gct gga cag att gga caa gac gct tcg ggc gtg aca gac cct     144
Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro
        35                  40                  45

gcc tac gag aaa cag gtt gcc caa gca ttc gcc aat ctg cga gct tgc     192
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
    50                  55                  60

ctt gct gca gtt gga gcc act tca aac gac gtc acc aag ctc aat tac     240
Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr
65                  70                  75                  80

tac atc gtc gac tac gcc ccg agc aaa ctc acc gca att gga gat ggg     288
Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
                85                  90                  95

ctg aag gct acc ttt gcc ctt gac agg ctc cct cct tgc acg ctg gtg     336
Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
            100                 105                 110

cca gtg tcg gcc ttg tct tca cct gaa tac ctc ttt gag gtt gat gcc     384
Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
        115                 120                 125

acg gcg ctg gtg ccg gga cac acg acc cca gac aac gtt gcg gac gtg     432
Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val
```

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    130                 135                 140

gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc      432
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
145                 150                 155                 160

cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta      528
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
                165                 170                 175

ggg gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg act atc      576
Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile
            180                 185                 190

aac gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta      624
Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val
        195                 200                 205

tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg      672
Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr
    210                 215                 220

act gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct      720
Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala
225                 230                 235                 240

cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg      768
Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala
                245                 250                 255

gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa      816
Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln
            260                 265                 270

gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc      864
Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe
        275                 280                 285

gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta      912
Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val
    290                 295                 300

gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc      960
Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile
305                 310                 315                 320

agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt     1008
Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser
                325                 330                 335

aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa     1056
Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys
            340                 345                 350

aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca     1104
Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro
        355                 360                 365
```

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ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca      1152
Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala
    370                 375                 380

tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa      1200
Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys
385                 390                 395                 400

aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt      1248
Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe
                405                 410                 415

tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc      1296
Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile
            420                 425                 430

ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg      1344
Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp
        435                 440                 445

cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc      1392
Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile
    450                 455                 460

tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att      1440
Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile
465                 470                 475                 480

acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc      1488
Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser
                485                 490                 495

aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac      1536
Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr
            500                 505                 510

gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc      1584
Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile
        515                 520                 525

gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat      1632
Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr
    530                 535                 540

ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc      1680
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe
545                 550                 555                 560

aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg      1728
Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly
                565                 570                 575

tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt      1776
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val
            580                 585                 590
```

gtg gct agc ctg gtg cca gca gca tag 1803
Val Ala Ser Leu Val Pro Ala Ala
595 600

<210> 23
<211> 600
<212> PRT
<213> Exophiala spinifera

<400> 23

Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro
1 5 10 15

Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val
20 25 30

Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro
35 40 45

Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
50 55 60

Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr
65 70 75 80

Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
85 90 95

Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
100 105 110

Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
115 120 125

Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val
130 135 140

Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
145 150 155 160

Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
165 170 175

Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile

```
            180                 185                 190

Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val
        195                 200                 205

Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr
    210                 215                 220

Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala
225                 230                 235                 240

Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala
                245                 250                 255

Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln
            260                 265                 270

Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe
        275                 280                 285

Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val
    290                 295                 300

Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile
305                 310                 315                 320

Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser
                325                 330                 335

Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys
            340                 345                 350

Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro
        355                 360                 365

Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala
    370                 375                 380

Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys
385                 390                 395                 400

Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe
                405                 410                 415
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Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile
420 425 430

Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp
435 440 445

Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile
450 455 460

Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile
465 470 475 480

Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser
485 490 495

Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr
500 505 510

Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile
515 520 525

Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr
530 535 540

Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe
545 550 555 560

Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly
565 570 575

Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val
580 585 590

Val Ala Ser Leu Val Pro Ala Ala
595 600

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<211> 3003
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<220>
<223> K:trAPAO (Exophiala spinifera)

<400> 24

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atg gcc aac aag cac ctg agc ctc tcc ctc ttc ctc gtg ctc ctc ggc      48
Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly
1               5                   10                  15

ctc tcc gcc tcc ctc gcc agc ggc gct cct act gtc aag att gat gct      96
Leu Ser Ala Ser Leu Ala Ser Gly Ala Pro Thr Val Lys Ile Asp Ala
            20                  25                  30

ggg atg gtg gtc ggc acg act act act gtc ccc ggc acc act gcg acc     144
Gly Met Val Val Gly Thr Thr Thr Thr Val Pro Gly Thr Thr Ala Thr
        35                  40                  45

gtc agc gag ttc ttg ggc gtt cct ttt gcc gcc tct ccg aca cga ttt     192
Val Ser Glu Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe
    50                  55                  60

gcg cct cct act cgt ccc gtg cct tgg tca acg cct ttg caa gcc act     240
Ala Pro Pro Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr
65                  70                  75                  80

gca tat ggt cca gca tgc cct caa caa ttc aat tac ccc gaa gaa ctc     288
Ala Tyr Gly Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu
                85                  90                  95

cgt gag att acg atg gcc tgg ttc aat aca ccg ccc ccg tca gct ggt     336
Arg Glu Ile Thr Met Ala Trp Phe Asn Thr Pro Pro Pro Ser Ala Gly
```

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                100                 105                 110

gaa agt gag gac tgc ctg aac ctc aac atc tac gtc cca gga act gag      336
Glu Ser Glu Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu
        115                 120                 125

aac aca aac aaa gcc gtc atg gtt tgg ata tac ggt gga gcg ctg gaa      432
Asn Thr Asn Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu
    130                 135                 140

tat ggt tgg aat tca ttc cac ctt tac gac ggg gct agt ttc gca gcc      480
Tyr Gly Trp Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala
145                 150                 155                 160

aat cag gat gtc atc gcc gtg acc atc aac tac aga acg aac att ctg      528
Asn Gln Asp Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu
                165                 170                 175

ggg ttc cct gct gcc cct cag ctt cca ata aca gag cga aat ctg ggg      576
Gly Phe Pro Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly
            180                 185                 190

ttc cta gac caa agg ttt gct ttg gat tgg gta cag cgg aac atc gca      624
Phe Leu Asp Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala
        195                 200                 205

gcc ttt ggc ggt gat cct cga aag gtc aca ata ttt ggg cag agt gcg      672
Ala Phe Gly Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala
    210                 215                 220

ggg ggc aga agt gtc gac gtc ctc ttg acg tct atg cca cac aac cca      720
Gly Gly Arg Ser Val Asp Val Leu Leu Thr Ser Met Pro His Asn Pro
225                 230                 235                 240

ccc ttc cga gca gca atc atg gag tcc ggt gtg gct aac tac aac ttc      768
Pro Phe Arg Ala Ala Ile Met Glu Ser Gly Val Ala Asn Tyr Asn Phe
                245                 250                 255

ccc aag gga gat ttg tcc gaa cct tgg aac acc act gtt caa gct ctc      816
Pro Lys Gly Asp Leu Ser Glu Pro Trp Asn Thr Thr Val Gln Ala Leu
            260                 265                 270

aac tgt acc acc agt atc gac atc ttg agt tgt atg aga aga gtc gat      864
Asn Cys Thr Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp
        275                 280                 285

ctc gcc act ctg atg aac acg atc gag caa ctc gga ctt ggg ttt gag      912
Leu Ala Thr Leu Met Asn Thr Ile Glu Gln Leu Gly Leu Gly Phe Glu
    290                 295                 300

tac acg ttg gac aac gta acg gct gtg tac cgt tct gaa acg gct cgc      960
Tyr Thr Leu Asp Asn Val Thr Ala Val Tyr Arg Ser Glu Thr Ala Arg
305                 310                 315                 320

acg act ggt gac att gct cgt gta cct gtt ctc gtc ggg acg gtg gcc     1008
Thr Thr Gly Asp Ile Ala Arg Val Pro Val Leu Val Gly Thr Val Ala
                325                 330                 335
```

```
aac gac gga ctt ctc ttt gtc ctc ggg gag aat gac acc caa gca tat      1056
Asn Asp Gly Leu Leu Phe Val Leu Gly Glu Asn Asp Thr Gln Ala Tyr
            340                 345                 350

ctc gag gag gca atc ccg aat cag ccc gac ctt tac cag act ctc ctt      1104
Leu Glu Glu Ala Ile Pro Asn Gln Pro Asp Leu Tyr Gln Thr Leu Leu
        355                 360                 365

gga gca tat ccc att gga tcc cca ggg atc gga tcg ctt caa gat cag      1152
Gly Ala Tyr Pro Ile Gly Ser Pro Gly Ile Gly Ser Leu Gln Asp Gln
    370                 375                 380

att gcc gcc att gag acc gag gta aga ttc cag tgt ctt tct gcc atc      1200
Ile Ala Ala Ile Glu Thr Glu Val Arg Phe Gln Cys Leu Ser Ala Ile
385                 390                 395                 400

gtg gct cag gat tcc cgg aat cgg ggt atc cct tct tgg cgc tac tac      1248
Val Ala Gln Asp Ser Arg Asn Arg Gly Ile Pro Ser Trp Arg Tyr Tyr
                405                 410                 415

tac aat gcg acc ttt gag aat ctg gag ctt ttc cct gtg tcc gaa gtg      1296
Tyr Asn Ala Thr Phe Glu Asn Leu Glu Leu Phe Pro Val Ser Glu Val
            420                 425                 430

tac cac agc tct gaa gtc ggg atg gtg ttt ggc acg tat cct gtc gca      1344
Tyr His Ser Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala
        435                 440                 445

agt gcg acc gcc ttg gag gcc cag acg agc aaa tac atg cag ggt gcc      1392
Ser Ala Thr Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly Ala
    450                 455                 460

tgg gcg gcc ttt gcc aaa aac ccc atg aat ggg cct gtg tgg aaa caa      1440
Trp Ala Ala Phe Ala Lys Asn Pro Met Asn Gly Pro Val Trp Lys Gln
465                 470                 475                 480

gtg ccg aat gtc gcg gcg ctt ggc tca cca ggc aaa gcc atc cag gtt      1488
Val Pro Asn Val Ala Ala Leu Gly Ser Pro Gly Lys Ala Ile Gln Val
                485                 490                 495

gac gtc tct cca gcg aca ata gac caa cga tgt gcc ttg tac acg cgt      1536
Asp Val Ser Pro Ala Thr Ile Asp Gln Arg Cys Ala Leu Tyr Thr Arg
            500                 505                 510

tat tat act gag ttg ggc aca atc gcg ccg agg aca ttt ggc gga ggc      1584
Tyr Tyr Thr Glu Leu Gly Thr Ile Ala Pro Arg Thr Phe Gly Gly Gly
        515                 520                 525

agc ggc gga ggc agc ggc gga ggc agc aaa gac aac gtt gcg gac gtg      1632
Ser Gly Gly Gly Ser Gly Gly Gly Ser Lys Asp Asn Val Ala Asp Val
    530                 535                 540

gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc      1680
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
545                 550                 555                 560
```

```
cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta      1728
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
                565                 570                 575

ggg gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg act atc      1776
Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile
            580                 585                 590

aac gac ctc ggc gct gcg tgg atc aat gat agc aac caa agc gaa gta      1824
Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val
        595                 600                 605

tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg      1872
Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr
    610                 615                 620

act gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct      1920
Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala
625                 630                 635                 640

cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg      1968
Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala
                645                 650                 655

gaa ctc ttc ccc gta tgg tct cag ctg atc gaa gag cat agc ttt caa      2016
Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln
            660                 665                 670

gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc      2064
Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe
        675                 680                 685

gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta      2112
Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val
    690                 695                 700

gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc      2160
Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile
705                 710                 715                 720

agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt      2208
Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser
                725                 730                 735

aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa      2256
Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys
            740                 745                 750

aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca      2304
Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro
        755                 760                 765

ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca      2352
Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala
    770                 775                 780

tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa      2400
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Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys
785                 790                 795                 800

aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt      2448
Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe
                805                 810                 815

tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc      2496
Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile
            820                 825                 830

ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg      2544
Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp
        835                 840                 845

cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tct gac ccc atc      2592
Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile
    850                 855                 860

tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att      2640
Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile
865                 870                 875                 880

acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc      2688
Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser
                885                 890                 895

aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac      2736
Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr
            900                 905                 910

gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc      2784
Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile
        915                 920                 925

gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat      2832
Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr
    930                 935                 940

ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc      2880
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe
945                 950                 955                 960

aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg      2928
Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly
                965                 970                 975

tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt      2976
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val
            980                 985                 990

gtg gct agc ctg gtg cca gca gca  tag                                3003
Val Ala Ser Leu Val Pro Ala Ala
        995                 1000
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<211> 1000
<212> PRT
<213> unknown

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<222> 73)..(1575)
<223> espl mat

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<221> misc_feature
<222> (1576)..(1611)
<223> spacer sequence

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<222> (1612)..(3000)
<223> P:trAPAO

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<222> (1612)..(1614)
<223> extra lysine

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Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly
1 5 10 15

Leu Ser Ala Ser Leu Ala Ser Gly Ala Pro Thr Val Lys Ile Asp Ala
20 25 30

Gly Met Val Val Gly Thr Thr Thr Thr Val Pro Gly Thr Thr Ala Thr
35 40 45

Val Ser Glu Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe
50 55 60

Ala Pro Pro Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr
65 70 75 80

Ala Tyr Gly Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu
85 90 95

Arg Glu Ile Thr Met Ala Trp Phe Asn Thr Pro Pro Pro Ser Ala Gly
100 105 110

Glu Ser Glu Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu
115 120 125

Asn Thr Asn Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu
130 135 140

Tyr Gly Trp Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala
145 150 155 160

Asn Gln Asp Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu
165 170 175

Gly Phe Pro Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly
180 185 190

Phe Leu Asp Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala
195 200 205

Ala Phe Gly Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala
210 215 220

Gly Gly Arg Ser Val Asp Val Leu Leu Thr Ser Met Pro His Asn Pro
225 230 235 240

Pro Phe Arg Ala Ala Ile Met Glu Ser Gly Val Ala Asn Tyr Asn Phe
245 250 255

Pro Lys Gly Asp Leu Ser Glu Pro Trp Asn Thr Thr Val Gln Ala Leu
260 265 270

Asn Cys Thr Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp
275 280 285

Leu Ala Thr Leu Met Asn Thr Ile Glu Gln Leu Gly Leu Gly Phe Glu
290 295 300

Tyr Thr Leu Asp Asn Val Thr Ala Val Tyr Arg Ser Glu Thr Ala Arg
305 310 315 320

Thr Thr Gly Asp Ile Ala Arg Val Pro Val Leu Val Gly Thr Val Ala
325 330 335

Asn Asp Gly Leu Leu Phe Val Leu Gly Glu Asn Asp Thr Gln Ala Tyr

340 345 350

Leu Glu Glu Ala Ile Pro Asn Gln Pro Asp Leu Tyr Gln Thr Leu Leu
355 360 365

Gly Ala Tyr Pro Ile Gly Ser Pro Gly Ile Gly Ser Pro Gln Asp Gln
370 375 380

Ile Ala Ala Ile Glu Thr Glu Val Arg Phe Gln Cys Pro Ser Ala Ile
385 390 395 400

Val Ala Gln Asp Ser Arg Asn Arg Gly Ile Pro Ser Trp Arg Tyr Tyr
405 410 415

Tyr Asn Ala Thr Phe Glu Asn Leu Glu Leu Phe Pro Gly Ser Glu Val
420 425 430

Tyr His Ser Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala
435 440 445

Ser Ala Thr Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly Ala
450 455 460

Trp Ala Ala Phe Ala Lys Asn Pro Met Asn Gly Pro Gly Trp Lys Gln
465 470 475 480

Val Pro Asn Val Ala Ala Leu Gly Ser Pro Gly Lys Ala Ile Gln Val
485 490 495

Asp Val Ser Pro Ala Thr Ile Asp Gln Arg Cys Ala Leu Tyr Thr Arg
500 505 510

Tyr Tyr Thr Glu Leu Gly Thr Ile Ala Pro Arg Thr Phe Gly Gly Gly
515 520 525

Ser Gly Gly Gly Ser Gly Gly Gly Ser Lys Asp Asn Val Ala Asp Val
530 535 540

Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
545 550 555 560

Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
565 570 575

Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile
580 585 590

Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val
595 600 605

Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr
610 615 620

Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala
625 630 635 640

Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala
645 650 655

Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln
660 665 670

Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe
675 680 685

Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val
690 695 700

Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile
705 710 715 720

Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser
725 730 735

Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys
740 745 750

Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro
755 760 765

Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala
770 775 780

Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys
785 790 795 800

Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe
805 810 815

Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile
820 825 830

Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp
835 840 845

Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile
850 855 860

Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile
865 870 875 880

Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser
885 890 895

Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr
900 905 910

Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile
915 920 925

Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr
930 935 940

Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe
945 950 955 960

Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly
965 970 975

Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val
980 985 990

Val Ala Ser Leu Val Pro Ala Ala
995 1000

<210> 26
<211> 2976
<212> DNA
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atg gcc aac aag cac ctg agc ctc tcc ctc ttc ctc gtg ctc ctc ggc       48
Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly
                -20                 -15                 -10

ctc tcc gcc tcc ctc gcc agc ggc acg gat ttt ccg gtc cgc agg acc       96
Leu Ser Ala Ser Leu Ala Ser Gly Thr Asp Phe Pro Val Arg Arg Thr
            -5              -1  1               5

gat ctg ggc cag gtt cag gga ctg gcc ggg gac gtg atg agc ttt cgc      144
Asp Leu Gly Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg
    10                  15                  20

gga ata ccc tat gca gcg ccg ccg gtg ggc ggg ctg cgt tgg aag ccg      192
Gly Ile Pro Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro
25                  30                  35                  40

ccc caa cac gcc cgg ccc tgg gcg ggc gtt cgc ccc gcc acc caa ttt      240
```

```
Pro Gln His Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe
                45                  50                  55

ggc tcc gac tgc ttc ggc gcg gcc tat ctt cgc aaa ggc agc ctc gcc      288
Gly Ser Asp Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala
            60                  65                  70

ccc ggc gtg agc gag gac tgt ctt tac ctc aac gta tgg gcg ccg tca      336
Pro Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser
        75                  80                  85

ggc gct aaa ccc ggc cag tac ccc gtc atg gtc tgg gtc tac ggc ggc      384
Gly Ala Lys Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly
    90                  95                  100

ggc ttc gcc agc ggc ggc acg gcc gcc atg ccc tac tac gac ggc gag      432
Gly Phe Ala Ser Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu
105                 110                 115                 120

ctt gcg cga cag ggc gtc gtc gtg gtg acg ttt aac tat cgg acg aac      480
Leu Ala Arg Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn
                125                 130                 135

atc ctg ggc ttt ttc gcc cat ccc ggt ctc tcg cgc gag agc ccc acc      528
Ile Leu Gly Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr
            140                 145                 150

gga act tcg ggc aac tac ggc cta ctc gac att ctc gcc gct ctt cgg      576
Gly Thr Ser Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg
        155                 160                 165

tgg gtg cag agc aac gcc cgc gcc ttc gga ggg gac ccc ggc cga gtg      624
Trp Val Gln Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val
    170                 175                 180

acg gtc ttt ggt gaa tcg gcc gga gcg agc gcg atc gga ctt ctg ctc      672
Thr Val Phe Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu
185                 190                 195                 200

acc tcg ccg ctg agc aag ggt ctc ttc cgt ggc gct atc ctc gaa agt      720
Thr Ser Pro Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser
                205                 210                 215

cca ggg ctg acg cga ccg ctc gcg acg ctc gcc gac agc gcc gcc tcg      768
Pro Gly Leu Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser
            220                 225                 230

ggc gag cgc ctc gac gcc gat ctt tcg cga ctg cgc tcg acc gac cca      816
Gly Glu Arg Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro
        235                 240                 245

gcc acc ctg atg gcg cgc gcc gac gcg gcc cgc ccg gca tcg cgg gac      864
Ala Thr Leu Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp
    250                 255                 260

ctg cgc agg ccg cgt ccg acc gga ccg atc gtc gat ggc cat gtg ctg      912
Leu Arg Arg Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu
```

```
265                 270                 275                 280

ccg cag acc gac agc ggg gcg atc gcg gcg ggt cag ctg gcg ccg gtt      960
Pro Gln Thr Asp Ser Ala Ala Ile Ala Ala Gly Gln Leu Ala Pro Val
                285                 290                 295

cgg gtc ctg atc gga acc aat gcc gac gaa ggt cgc gcc ttc ctc ggg     1008
Arg Val Leu Ile Gly Thr Asn Ala Asp Glu Gly Arg Ala Phe Leu Gly
            300                 305                 310

cgc gcg ccg atg gag acg ccg gcg gac tac cag gcc tat ctg gag gcg     1056
Arg Ala Pro Met Glu Thr Pro Ala Asp Tyr Gln Ala Tyr Leu Glu Ala
        315                 320                 325

cag ttt ggc gac cag gcc gcc gcg gtg gcg gcg tgc tat ccg ctc gac     1104
Gln Phe Gly Asp Gln Ala Ala Ala Val Ala Ala Cys Tyr Pro Leu Asp
    330                 335                 340

ggc cgg gcc acg ccc aag gaa atg gtc ggg cgc atc ttc ggc gac aat     1152
Gly Arg Ala Thr Pro Lys Glu Met Val Ala Arg Ile Phe Gly Asp Asn
345                 350                 355                 360

cag ttc aat cgg ggg gtc tcg gcc ttc tcg gaa gcg ctt gtg cgc cag     1200
Gln Phe Asn Arg Gly Val Ser Ala Phe Ser Glu Ala Leu Val Arg Gln
                365                 370                 375

ggc gcg ccc gtg tgg cgt tat cag ttc aac ggt aat acc gag ggt gga     1248
Gly Ala Pro Val Trp Arg Tyr Gln Phe Asn Gly Asn Thr Glu Gly Gly
            380                 385                 390

agg gcg ccg gct acc cac gga gcc gaa att ccc tac gtt ttc ggg gtg     1296
Arg Ala Pro Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val
        395                 400                 405

ttc aag ctc gac gag ttg ggt ctg ttc gat tgg ccg ccc gag ggg ccc     1344
Phe Lys Leu Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro
    410                 415                 420

acg ccc gcc gac cgt gcg ctg ggc caa ctg atg tcc tcc gcc tgg gtc     1392
Thr Pro Ala Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val
425                 430                 435                 440

cgg ttc gcc aag aat ggc gac ccc gcc ggg gac gcc ctt acc tgg cct     1440
Arg Phe Ala Lys Asn Gly Asp Pro Ala Gly Asp Ala Leu Thr Trp Pro
                445                 450                 455

gcc tat tct acg ggc aag tcg acc atg aca ttc ggt ccc gag ggc cgc     1488
Ala Tyr Ser Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg
            460                 465                 470

gcg gcg gtg gtg tcg ccc gga cct tcc atc ccc cct tgc gcg gat ggc     1536
Ala Ala Val Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly
        475                 480                 485

gcc aag gcg ggg ggc gga ggc agc ggc gga ggc agc ggc gga ggc agc     1584
Ala Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
    490                 495                 500
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aaa gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt      1632
Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
505                 510                 515                 520

ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt      1680
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val
                525                 530                 535

ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg      1728
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
            540                 545                 550

ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat      1776
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
        555                 560                 565

gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg      1824
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
    570                 575                 580

gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa      1872
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
585                 590                 595                 600

gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag      1920
Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
                605                 610                 615

gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg      1968
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu
            620                 625                 630

atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag      2016
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
        635                 640                 645

cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac      2064
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
    650                 655                 660

ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc      2112
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu
665                 670                 675                 680

ggt gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc      2160
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile
                685                 690                 695

aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc      2208
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly
            700                 705                 710

ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc      2256
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala
        715                 720                 725
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atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc      2304
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val
    730                 735                 740

gct gaa att gag cag tcg gca tct ggc tgt aca gta cga tgg gcc tcg      2352
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser
745                 750                 755                 760

ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc      2400
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr
                765                 770                 775

ttg tat ccc acc ttg aga ttt tca cca cct ctt ccc gcc gag aag caa      2448
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
            780                 785                 790

gca ttg ggg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc      2496
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
        795                 800                 805

gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc      2544
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
    810                 815                 820

caa tcg agc tgt gac ccc atc tcc ttt gcc aga gat acc agc atc gac      2592
Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
825                 830                 835                 840

gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga      2640
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
                845                 850                 855

agg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg      2688
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
            860                 865                 870

gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag      2736
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
        875                 880                 885

ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa      2784
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
    890                 895                 900

gga gct ccg agc gcc gtc tat ggc ctg aac gat ctc atc aca ctg ggt      2832
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
905                 910                 915                 920

tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag      2880
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
                925                 930                 935

acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt      2928
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
            940                 945                 950

caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag      2976
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Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
955 960 965

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Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly
-20 -15 -10

Leu Ser Ala Ser Leu Ala Ser Gly Thr Asp Phe Pro Val Arg Arg Thr
-5 -1 1 5

Asp Leu Gly Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg
10 15 20

Gly Ile Pro Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro
25 30 35 40

Pro Gln His Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe
45 50 55

Gly Ser Asp Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala
60 65 70

Pro Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser
75 80 85

Gly Ala Lys Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly
90 95 100

Gly Phe Ala Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Gln Ala
105 110 115 120

Leu Ala Arg Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn
125 130 135

Ile Leu Gly Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr
140 145 150

Gly Thr Ser Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg
155 160 165

Trp Val Gln Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val
170 175 180

Thr Val Phe Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu
185 190 195 200

Thr Ser Pro Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser
205 210 215

Pro Gly Leu Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser
220 225 230

Gly Glu Arg Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro
235 240 245

Ala Thr Leu Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp
250 255 260

Leu Arg Arg Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu
265 270 275 280

Pro Gln Thr Asp Ser Ala Ala Ile Ala Ala Gly Gln Leu Ala Pro Val
285 290 295

Arg Val Leu Ile Gly Thr Asn Ala Asp Glu Gly Arg Ala Phe Leu Gly
300 305 310

Arg Ala Pro Met Glu Thr Pro Ala Asp Tyr Gln Ala Tyr Leu Glu Ala

315 320 325

Gln Phe Gly Asp Gln Ala Ala Ala Val Ala Ala Cys Tyr Pro Leu Asp
330 335 340

Gly Arg Ala Thr Pro Lys Glu Met Val Ala Arg Ile Phe Gly Asp Asn
345 350 355 360

Gln Phe Asn Arg Gly Val Ser Ala Phe Ser Glu Ala Leu Val Arg Gln
365 370 375

Gly Ala Pro Val Trp Arg Tyr Gln Phe Asn Gly Asn Thr Glu Gly Gly
380 385 390

Arg Ala Pro Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val
395 400 405

Phe Lys Leu Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro
410 415 420

Thr Pro Ala Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val
425 430 435 440

Arg Phe Ala Lys Asn Gly Asp Pro Ala Gly Asp Ala Leu Thr Trp Pro
445 450 455

Ala Tyr Ser Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg
460 465 470

Ala Ala Val Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly
475 480 485

Ala Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
490 495 500

Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
505 510 515 520

Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val
525 530 535

Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
540 545 550

Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
555 560 565

Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
570 575 580

Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
585 590 595 600

Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
605 610 615

Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu
620 625 630

Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
635 640 645

Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
650 655 660

Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu
665 670 675 680

Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile
685 690 695

Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly
700 705 710

Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala
715 720 725

Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val
730 735 740

Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser
745 750 755 760

Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr
765 770 775

Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
730 735 790

Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
795 800 805

Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
810 815 820

Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
825 830 835 840

Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
845 850 855

Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
860 865 870

Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
875 880 885

Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
890 895 900

Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
905 910 915 920

Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
925 930 935

Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
940 945 950

Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
955 960 965

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<222> (2227)..(3615)
<223> KirAPA0

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<223> extra lysine

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Met Ser Pro Ile Leu  Gly Tyr Trp Lys Ile  Lys Gly Leu Val Gln
                -225                -220                -215

ccc act cga ctt ctt  ttg gaa tat ctt gaa  gaa aaa tat gaa gag          90
Pro Thr Arg Leu Leu  Leu Glu Tyr Leu Glu  Glu Lys Tyr Glu Glu
                -210                -205                -200

cat ttg tat gag cgc  gat gaa ggt gat aaa  tgg cga aac aaa aag         135
His Leu Tyr Glu Arg  Asp Glu Gly Asp Lys  Trp Arg Asn Lys Lys
                -195                -190                -185

ttt gaa ttg ggt ttg  gag ttt ccc aat ctt  cct tat tat att gat         180
Phe Glu Leu Gly Leu  Glu Phe Pro Asn Leu  Pro Tyr Tyr Ile Asp
                -180                -175                -170

ggt gat gtt aaa tta  aca cag tct atg gcc  atc ata cgt tat ata         225
Gly Asp Val Lys Leu  Thr Gln Ser Met Ala  Ile Ile Arg Tyr Ile
                -165                -160                -155

gct gac aag cac aac  atg ttg ggt ggt tgt  cca aaa gag cgt gca         270
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Ala Asp Lys His Asn  Met Leu Gly Gly Cys  Pro Lys Glu Arg Ala
                -150                 -145                 -140

gag att tca atg ctt  gaa gga gcg gtt ttg  gat att aga tac ggt        315
Glu Ile Ser Met Leu  Glu Gly Ala Val Leu  Asp Ile Arg Tyr Gly
                -135                 -130                 -125

gtt tcg aga att gca  tat agt aaa gac ttt  gaa act ctc aaa gtt        360
Val Ser Arg Ile Ala  Tyr Ser Lys Asp Phe  Glu Thr Leu Lys Val
                -120                 -115                 -110

gat ttt ctt agc aag  cta cct gaa atg ttg  aaa atg ttc gaa gat cgt    408
Asp Phe Leu Ser Lys  Leu Pro Glu Met Leu  Lys Met Phe Glu Asp Arg
                -105                 -100                 -95

tta tgt cat aaa aca tat tta aat ggt gat cat gta acc cat cct gac      456
Leu Cys His Lys Thr Tyr Leu Asn Gly Asp His Val Thr His Pro Asp
            -90                  -85                  -80

ttc atg ttg tat gac gct ctt gat gtt gtt tta tac atg gac cca atg      504
Phe Met Leu Tyr Asp Ala Leu Asp Val Val Leu Tyr Met Asp Pro Met
        -75                  -70                  -65

tgc ctg gat gcg ttc cca aaa tta gtt tgt ttt aaa aaa cgt att gaa      552
Cys Leu Asp Ala Phe Pro Lys Leu Val Cys Phe Lys Lys Arg Ile Glu
    -60                  -55                  -50

gct atc cca caa att gat aag tac ttg aaa tcc agc aag tat ata gca      600
Ala Ile Pro Gln Ile Asp Lys Tyr Leu Lys Ser Ser Lys Tyr Ile Ala
-45                  -40                  -35                  -30

tgg cct ttg cag ggc tgg caa gcc acg ttt ggt ggt ggc gac cat cct      648
Trp Pro Leu Gln Gly Trp Gln Ala Thr Phe Gly Gly Gly Asp His Pro
                -25                  -20                  -15

cca aaa tcg gat ctg gtt ccg cgt gga tcc ccg gaa ttc gct cct act      696
Pro Lys Ser Asp Leu Val Pro Arg Gly Ser Pro Glu Phe Ala Pro Thr
            -10                  -5                   -1  1

gtc aag att gat gct ggg atg gtg gtc ggc acg act act act gtc ccc      744
Val Lys Ile Asp Ala Gly Met Val Val Gly Thr Thr Thr Thr Val Pro
    5                   10                  15

ggc acc act gcg acc gtc agc gag ttc ttg ggc gtt cct ttt gcc gcc      792
Gly Thr Thr Ala Thr Val Ser Glu Phe Leu Gly Val Pro Phe Ala Ala
20                  25                  30                  35

tct ccg aca cga ttt gcg cct cct act cgt ccc gtg cct tgg tca acg      840
Ser Pro Thr Arg Phe Ala Pro Pro Thr Arg Pro Val Pro Trp Ser Thr
                40                  45                  50

cct ttg caa gcc act gca tat ggt cca gca tgc cct caa caa ttc aat      888
Pro Leu Gln Ala Thr Ala Tyr Gly Pro Ala Cys Pro Gln Gln Phe Asn
            55                  60                  65

tac ccc gaa gaa ctc cgt gag att acg atg gcc tgg ttc aat aca ccg      936
Tyr Pro Glu Glu Leu Arg Glu Ile Thr Met Ala Trp Phe Asn Thr Pro
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        70                  75                  80

ccc ccg tca gct ggt gaa agt gag gac tgc ctg aac ctc aac atc tac      984
Pro Pro Ser Ala Gly Glu Ser Glu Asp Cys Leu Asn Leu Asn Ile Tyr
    85                  90                  95

gtc cca gga act gag aac aca aac aaa gcc gtc atg gtt tgg ata tac     1032
Val Pro Gly Thr Glu Asn Thr Asn Lys Ala Val Met Val Trp Ile Tyr
100                 105                 110                 115

ggt gga ggg ctg gaa tat ggt tgg aat tca ttc cac ctt tac gac ggg     1080
Gly Gly Ala Leu Glu Tyr Gly Trp Asn Ser Phe His Leu Tyr Asp Gly
                120                 125                 130

gct agt ttc gca gcc aat cag gat gtc atc gcc gtg acc atc aac tac     1128
Ala Ser Phe Ala Ala Asn Gln Asp Val Ile Ala Val Thr Ile Asn Tyr
            135                 140                 145

aga acg aac att ctg ggg ttc cct gct gcc cct cag ctt cca ata aca     1176
Arg Thr Asn Ile Leu Gly Phe Pro Ala Ala Pro Gln Leu Pro Ile Thr
        150                 155                 160

cag cga aat ctg ggg ttc cta gac caa agg ttt gct ttg gat tgg gta     1224
Gln Arg Asn Leu Gly Phe Leu Asp Gln Arg Phe Ala Leu Asp Trp Val
    165                 170                 175

cag cgg aac atc gca gcc ttt ggc ggt gat cct cga aag gtc aca ata     1272
Gln Arg Asn Ile Ala Ala Phe Gly Gly Asp Pro Arg Lys Val Thr Ile
180                 185                 190                 195

ttt ggg cag agt gcg gcg ggc agc agt gtc gac gtc ctc ttg acg tct     1320
Phe Gly Gln Ser Ala Gly Gly Arg Ser Val Asp Val Leu Leu Thr Ser
                200                 205                 210

atg cca cac aac cca ccc ttc cga gca gca atc atg gag tcc ggt gtg     1368
Met Pro His Asn Pro Pro Phe Arg Ala Ala Ile Met Glu Ser Gly Val
            215                 220                 225

gct aac tac aac ttc ccc aag gga gat ttg tcc gaa cct tgg aac acc     1416
Ala Asn Tyr Asn Phe Pro Lys Gly Asp Leu Ser Glu Pro Trp Asn Thr
        230                 235                 240

act gtt caa gct ctc aac tgt acc acc agt atc gac atc ttg agt tgt     1464
Thr Val Gln Ala Leu Asn Cys Thr Thr Ser Ile Asp Ile Leu Ser Cys
    245                 250                 255

atg aga aga gtc gat ctc gcc act ctg atg aac acg atc gag caa ctc     1512
Met Arg Arg Val Asp Leu Ala Thr Leu Met Asn Thr Ile Glu Gln Leu
260                 265                 270                 275

gga ctt ggg ttt gag tac acg ttg gac aac gta acg gct gtg tac cgt     1560
Gly Leu Gly Phe Glu Tyr Thr Leu Asp Asn Val Thr Ala Val Tyr Arg
                280                 285                 290

tct gaa acg gct cgc acg act ggt gac att gct cgt gta cct gtt ctc     1608
Ser Glu Thr Ala Arg Thr Thr Gly Asp Ile Ala Arg Val Pro Val Leu
            295                 300                 305
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gtc ggg acg gtg gcc aac gac gga ctt ctc ttt gtc ctc ggg gag aat      1656
Val Gly Thr Val Ala Asn Asp Gly Leu Leu Phe Val Leu Gly Glu Asn
        310                 315                 320

gac acc caa gca tat ctc gag gag gca atc ccg aat caa ccc gac ctt      1704
Asp Thr Gln Ala Tyr Leu Glu Glu Ala Ile Pro Asn Gln Pro Asp Leu
    325                 330                 335

tac cag act ctc ctt gga gca tat ccc att gga tcc cca ggg atc gga      1752
Tyr Gln Thr Leu Leu Gly Ala Tyr Pro Ile Gly Ser Pro Gly Ile Gly
340                 345                 350                 355

tcg cct caa gat cag att gcc gcc att gag acc gag gtc agg ttc cag      1800
Ser Pro Gln Asp Gln Ile Ala Ala Ile Glu Thr Glu Val Arg Phe Gln
                360                 365                 370

tgt cct tct gcc atc gtg gct cag gac tcc cgc aat cgc ggt atc cct      1848
Cys Pro Ser Ala Ile Val Ala Gln Asp Ser Arg Asn Arg Gly Ile Pro
            375                 380                 385

tct tgg cgc tac tac tac aat gcg acc ttt gag aat ctc gag ctt ttc      1896
Ser Trp Arg Tyr Tyr Tyr Asn Ala Thr Phe Glu Asn Leu Glu Leu Phe
        390                 395                 400

cct ggg tcc gaa gtg tac cac agc tct gaa gtc ggg atg gtg ttt ggc      1944
Pro Gly Ser Glu Val Tyr His Ser Ser Glu Val Gly Met Val Phe Gly
    405                 410                 415

acg tat cct gtc gca agt gcg acc gcc ttg gag gcc cag acg agc aaa      1992
Thr Tyr Pro Val Ala Ser Ala Thr Ala Leu Glu Ala Gln Thr Ser Lys
420                 425                 430                 435

tac atg cag ggt gcc tgg gcg gcc ttt gcc aaa aac ccc atg aat ggg      2040
Tyr Met Gln Gly Ala Trp Ala Ala Phe Ala Lys Asn Pro Met Asn Gly
                440                 445                 450

cct ggg tgg aaa caa gtg ccg aat gtc gcg gcg ctt ggc tca cca ggc      2088
Pro Gly Trp Lys Gln Val Pro Asn Val Ala Ala Leu Gly Ser Pro Gly
            455                 460                 465

aaa gcc atc cag gtt gac gtc tct cca gcg aca ata gac caa cga tgt      2136
Lys Ala Ile Gln Val Asp Val Ser Pro Ala Thr Ile Asp Gln Arg Cys
        470                 475                 480

gcc ttg tac acg cct tat tat act gag ttg ggc aca atc gcg ccg agg      2184
Ala Leu Tyr Thr Arg Tyr Tyr Thr Glu Leu Gly Thr Ile Ala Pro Arg
    485                 490                 495

aca ttt ggc gga ggc agc ggc gga ggc agc ggc gga ggc agc aaa gac      2232
Thr Phe Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Lys Asp
500                 505                 510                 515

aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt ttg gag      2280
Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu
                520                 525                 530
```

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acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag      1323
Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu
            535                 540                 545

gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt ccc      1371
Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro
        550                 555                 560

ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac agc      1419
Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser
    565                 570                 575

aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag ggc      1467
Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly
580                 585                 590                 595

gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac ggt      1515
Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly
                600                 605                 610

aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag gtt      1563
Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val
            615                 620                 625

gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc gaa      1611
Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu
        630                 635                 640

gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg ctc      1659
Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu
    645                 650                 655

gac agt gtg agc ttc gcg cac tac tgt gag aag gaa ctg aac ttg cct      1707
Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro
660                 665                 670                 675

gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt gtg      1755
Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val
                680                 685                 690

gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag agt      1803
Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser
            695                 700                 705

gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg cag      1851
Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln
        710                 715                 720

tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc atg tca      1899
Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser
    725                 730                 735

aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa      1947
Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu
740                 745                 750                 755

att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc      1995
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Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala
                760                 765                 770

gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg tat      3048
Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr
            775                 780                 785

ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg      3096
Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu
        790                 795                 800

gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg      3144
Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp
    805                 810                 815

gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtt ctc caa tcg      3192
Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser
820                 825                 830                 835

agc tct gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat      3240
Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp
                840                 845                 850

cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cgg aag      3288
Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys
            855                 860                 865

tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac caa      3336
Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln
        870                 875                 880

ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc      3384
Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala
    885                 890                 895

aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga gct      3432
Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala
900                 905                 910                 915

ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg gcg      3480
Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala
                920                 925                 930

ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg tct      3528
Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser
            935                 940                 945

tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa cga      3576
Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg
        950                 955                 960

ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag               3618
Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
    965                 970                 975
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<211> 1205
<212> PRT
<213> Unknown

<220>
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<220>
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<222> (1)..(627)
<223> gst + polylinker

<220>
<221> misc_feature
<222> (1191)..(2226)
<223> spacer sequence

<220>
<221> misc_feature
<222> (2227)..(3615)
<223> K:trAPAO

<220>
<221> misc_feature
<222> (2227)..(2229)
<223> extra lysine

<400> 29

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln
-235 -230 -225

Pro Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu
-210 -205 -200

His Leu Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys
-195 -190 -185

Phe Glu Leu Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp
-180 -175 -170

Gly Asp Val Lys Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile
-165 -160 -155

Ala Asp Lys His Asn Met Leu Gly Gly Cys Pro Lys Glu Arg Ala
-150 -145 -140

Glu Ile Ser Met Leu Glu Gly Ala Val Leu Asp Ile Arg Tyr Gly
-135 -130 -125

Val Ser Arg Ile Ala Tyr Ser Lys Asp Phe Glu Thr Leu Lys Val
-120 -115 -110

Asp Phe Leu Ser Lys Leu Pro Glu Met Leu Lys Met Phe Glu Asp Arg
-105 -100 -95

Leu Cys His Lys Thr Tyr Leu Asn Gly Asp His Val Thr His Pro Asp
-90 -85 -80

Phe Met Leu Tyr Asp Ala Leu Asp Val Val Leu Tyr Met Asp Pro Met
-75 -70 -65

Cys Leu Asp Ala Phe Pro Lys Leu Val Cys Phe Lys Lys Arg Ile Glu
-60 -55 -50

Ala Ile Pro Gln Ile Asp Lys Tyr Leu Lys Ser Ser Lys Tyr Ile Ala
-45 -40 -35 -30

Trp Pro Leu Gln Gly Trp Gln Ala Thr Phe Gly Gly Gly Asp His Pro
-25 -20 -15

Pro Lys Ser Asp Leu Val Pro Arg Gly Ser Pro Glu Phe Ala Pro Thr
-10 -5 -1 1

Val Lys Ile Asp Ala Gly Met Val Val Gly Thr Thr Thr Thr Val Pro
5 10 15

Gly Thr Thr Ala Thr Val Ser Glu Phe Leu Gly Val Pro Phe Ala Ala
20 25 30 35

Ser Pro Thr Arg Phe Ala Pro Pro Thr Arg Pro Val Pro Trp Ser Thr
40 45 50

Pro Leu Gln Ala Thr Ala Tyr Gly Pro Ala Cys Pro Gln Gln Phe Asn
55 60 65

Tyr Pro Glu Glu Leu Arg Glu Ile Thr Met Ala Trp Phe Asn Thr Pro
70 75 80

Pro Pro Ser Ala Gly Glu Ser Glu Asp Cys Leu Asn Leu Asn Ile Tyr
85 90 95

Val Pro Gly Thr Glu Asn Thr Asn Lys Ala Val Met Val Trp Ile Tyr

100 105 110 115

Gly Gly Ala Leu Glu Tyr Gly Trp Asn Ser Phe His Leu Tyr Asp Gly
120 125 130

Ala Ser Phe Ala Ala Asn Gln Asp Val Ile Ala Val Thr Ile Asn Tyr
135 140 145

Arg Thr Asn Ile Leu Gly Phe Pro Ala Ala Pro Gln Leu Pro Ile Thr
150 155 160

Gln Arg Asn Leu Gly Phe Leu Asp Gln Arg Phe Ala Leu Asp Trp Val
165 170 175

Gln Arg Asn Ile Ala Ala Phe Gly Gly Asp Pro Arg Lys Val Thr Ile
180 185 190 195

Phe Gly Gln Ser Ala Gly Gly Arg Ser Val Asp Val Leu Leu Thr Ser
200 205 210

Met Pro His Asn Pro Pro Phe Arg Ala Ala Ile Met Glu Ser Gly Val
215 220 225

Ala Asn Tyr Asn Phe Pro Lys Gly Asp Leu Ser Glu Pro Trp Asn Thr
230 235 240

Thr Val Gln Ala Leu Asn Cys Thr Thr Ser Ile Asp Ile Leu Ser Cys
245 250 255

Met Arg Arg Val Asp Leu Ala Thr Leu Met Asn Thr Ile Glu Gln Leu
260 265 270 275

Gly Leu Gly Phe Glu Tyr Thr Leu Asp Asn Val Thr Ala Val Tyr Arg
280 285 290

Ser Glu Thr Ala Arg Thr Thr Gly Asp Ile Ala Arg Val Pro Val Leu
295 300 305

Val Gly Thr Val Ala Asn Asp Gly Leu Leu Phe Val Leu Gly Glu Asn
310 315 320

Asp Thr Gln Ala Tyr Leu Glu Glu Ala Ile Pro Asn Gln Pro Asp Leu
325 330 335

Tyr Gln Thr Leu Leu Gly Ala Tyr Pro Ile Gly Ser Pro Gly Ile Gly
340 345 350 355

Ser Pro Gln Asp Gln Ile Ala Ala Ile Glu Thr Glu Val Arg Phe Gln
360 365 370

Cys Pro Ser Ala Ile Val Ala Gln Asp Ser Arg Asn Arg Gly Ile Pro
375 380 385

Ser Trp Arg Tyr Tyr Tyr Asn Ala Thr Phe Glu Asn Leu Glu Leu Phe
390 395 400

Pro Gly Ser Glu Val Tyr His Ser Ser Glu Val Gly Met Val Phe Gly
405 410 415

Thr Tyr Pro Val Ala Ser Ala Thr Ala Leu Glu Ala Gln Thr Ser Lys
420 425 430 435

Tyr Met Gln Gly Ala Trp Ala Ala Phe Ala Lys Asn Pro Met Asn Gly
440 445 450

Pro Gly Trp Lys Gln Val Pro Asn Val Ala Ala Leu Gly Ser Pro Gly
455 460 465

Lys Ala Ile Gln Val Asp Val Ser Pro Ala Thr Ile Asp Gln Arg Cys
470 475 480

Ala Leu Tyr Thr Arg Tyr Tyr Thr Glu Leu Gly Thr Ile Ala Pro Arg
485 490 495

Thr Phe Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Lys Asp
500 505 510 515

Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu
520 525 530

Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu
535 540 545

Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro
550 555 560

Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser
565 570 575

Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly
580 585 590 595

Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly
600 605 610

Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val
615 620 625

Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu
630 635 640

Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu
645 650 655

Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro
660 665 670 675

Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val
680 685 690

Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser
695 700 705

Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln
710 715 720

Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser
725 730 735

Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu
740 745 750 755

Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala
760 765 770

Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr
775 780 785

Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu
790 795 800

Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp
805 810 815

Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser
820 825 830 835

Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp
840 845 850

Asn Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys
855 860 865

Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln
870 875 880

Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala
885 890 895

Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala
900 905 910 915

Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala
920 925 930

Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser
935 940 945

Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg
950 955 960

Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
965 970 975

<210> 30
<211> 3591
<212> DNA
<213> Unknown

<220>
<223> Orf of BEST1:K:trAPAO fusion pGEX-4T-1 (Exophiala spinifera)

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1)..(637)
gst + polylinker

mat_peptide
(638)..(2163)
BEST1 mature

misc_feature
(2164)..(2199)
spacer sequence

misc_feature
(2200)..(2553)
KirAPA0

CDS
(1)..(3558)

misc_feature
(2900)..(2902)
extra lysine

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atg tcc cct ata cta ggt tat tgg aaa att aag ggc ctt gtg caa 45
Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln
-225 -220 -215

ccc act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag 90
Pro Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu
-210 -205 -200

cat ttg tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag 135
His Leu Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys
-195 -190 -185

ttt gaa ttg ggt ttg gag ttt ccc aat ctt cct tat tat att gat 180
Phe Glu Leu Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp
-180 -175 -170

ggt gat gtt aaa tta aca cag tct atg gcc atc ata cgt tat ata 225
Gly Asp Val Lys Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile
-165 -160 -155

gct gac aag cac aac atg ttg ggt ggt tgt cca aaa gag cgt gca 270
Ala Asp Lys His Asn Met Leu Gly Gly Cys Pro Lys Glu Arg Ala

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                -150                -145                -140

gag att tca atg ctt  gaa gga gcg gtt ttg  gat att aga tac ggt        315
Glu Ile Ser Met Leu  Glu Gly Ala Val Leu  Asp Ile Arg Tyr Gly
                -135                -130                -125

gtt tcg aga att gca  tat agt aaa gac ttt  gaa act ctc aaa gtt        360
Val Ser Arg Ile Ala  Tyr Ser Lys Asp Phe  Glu Thr Leu Lys Val
                -120                -115                -110

gat ttt ctt agc aag  cta cct gaa atg ctg  aaa atg ttc gaa gat cgt    408
Asp Phe Leu Ser Lys  Leu Pro Glu Met Leu  Lys Met Phe Glu Asp Arg
                -105                -100                -95

tta tgt cat aaa acg tat tta aat ggt gat cat gta acc cat cct gac      456
Leu Cys His Lys Thr Tyr Leu Asn Gly Asp His Val Thr His Pro Asp
            -90                 -85                 -80

ttc atg ttg tat gac gct ctt gat gtt gtt tta tac atg gac cca atg      504
Phe Met Leu Tyr Asp Ala Leu Asp Val Val Leu Tyr Met Asp Pro Met
        -75                 -70                 -65

tgc ctg gat gcg ttc cca aaa tta gtt tgt ttt aaa aaa cgt att gaa      552
Cys Leu Asp Ala Phe Pro Lys Leu Val Cys Phe Lys Lys Arg Ile Glu
    -60                 -55                 -50

gct atc cca caa att gat aag tac ttg aaa tcc agc aag tat ata gca      600
Ala Ile Pro Gln Ile Asp Lys Tyr Leu Lys Ser Ser Lys Tyr Ile Ala
-45                 -40                 -35                 -30

tgg cct ttg cag ggc tgg caa gcc acg ttt ggt ggt ggc gac cat cct      648
Trp Pro Leu Gln Gly Trp Gln Ala Thr Phe Gly Gly Gly Asp His Pro
                -25                 -20                 -15

cca aaa tcg gat ctg gtt ccg cgt gga tcc ccg gaa ttc acg gat ttt      696
Pro Lys Ser Asp Leu Val Pro Arg Gly Ser Pro Glu Phe Thr Asp Phe
            -10                 -5                  -1  1

ccg gtc cgc agg acc gat ctg ggc cag gtt cag gga ctg gcc ggg gac      744
Pro Val Arg Arg Thr Asp Leu Gly Gln Val Gln Gly Leu Ala Gly Asp
    5                   10                  15

gtg atg agc ttt cgc gga ata ccc tat gca gcg ccg ccg gtg ggc ggg      792
Val Met Ser Phe Arg Gly Ile Pro Tyr Ala Ala Pro Pro Val Gly Gly
20                  25                  30                  35

ctg cgt tgg aag ccg ccc caa cac gcc cgg ccc tgg gcg ggc gtt cgc      840
Leu Arg Trp Lys Pro Pro Gln His Ala Arg Pro Trp Ala Gly Val Arg
                40                  45                  50

ccc gcc acc caa ttt ggc tcc gac tgc ttc ggc gcg gcc tat ctt cgc      888
Pro Ala Thr Gln Phe Gly Ser Asp Cys Phe Gly Ala Ala Tyr Leu Arg
            55                  60                  65

aaa ggc agc ctc gcc ccc ggc gtg agc gag gac tgt ctt tac ctc aac      936
Lys Gly Ser Leu Ala Pro Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn
        70                  75                  80
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gta tgg gcg ccg tca ggc gct aaa ccc ggc cag tac ccc gtc atg gtc      984
Val Trp Ala Pro Ser Gly Ala Lys Pro Gly Gln Tyr Pro Val Met Val
    85                  90                  95

tgg gtc tac ggc ggc ggc ttc gcc ggc ggc acg gcc gcc atg ccc tac     1032
Trp Val Tyr Gly Gly Gly Phe Ala Gly Gly Thr Ala Ala Met Pro Tyr
100                 105                 110                 115

tac gac ggc gag gcg ctt gcg cga cag ggc gtc gtc gtg gtg acg ttt     1080
Tyr Asp Gly Glu Ala Leu Ala Arg Gln Gly Val Val Val Val Thr Phe
                120                 125                 130

aac tat cgg acg aac atc ctg ggc ttt ttc gcc cat ccc ggt ctc tcg     1128
Asn Tyr Arg Thr Asn Ile Leu Gly Phe Phe Ala His Pro Gly Leu Ser
            135                 140                 145

cgc gag agc ccc acc gga act tcg ggc aac tac ggc cta ctc gac att     1176
Arg Glu Ser Pro Thr Gly Thr Ser Gly Asn Tyr Gly Leu Leu Asp Ile
        150                 155                 160

ctc gcc gct ctt cgg tgg gtg cag agc aac gcc cgc gcc ttc gga ggg     1224
Leu Ala Ala Leu Arg Trp Val Gln Ser Asn Ala Arg Ala Phe Gly Gly
    165                 170                 175

gac ccc ggc cga gtg acg gtc ttt ggt gaa tcg gcc gga gcg agc gcg     1272
Asp Pro Gly Arg Val Thr Val Phe Gly Glu Ser Ala Gly Ala Ser Ala
180                 185                 190                 195

atc gga ctt ctg ctc acc tcg ccg ctg agc aag ggt ctc ttc cgt ggc     1320
Ile Gly Leu Leu Leu Thr Ser Pro Leu Ser Lys Gly Leu Phe Arg Gly
                200                 205                 210

gct atc ctc gaa agt cca ggg ctg acg cga ccg ctc gcg acg ctc gcc     1368
Ala Ile Leu Glu Ser Pro Gly Leu Thr Arg Pro Leu Ala Thr Leu Ala
            215                 220                 225

gac agc gcc gcc tcg ggc gag cgc ctc gac gcc gat ctt tcg cga ctg     1416
Asp Ser Ala Ala Ser Gly Glu Arg Leu Asp Ala Asp Leu Ser Arg Leu
        230                 235                 240

cgc tcg acc gac ccg gcc acc ctg atg gcg cgc gcc gac gcg gcc cgc     1464
Arg Ser Thr Asp Pro Ala Thr Leu Met Ala Arg Ala Asp Ala Ala Arg
    245                 250                 255

ccg gca tcg cgg gac ctg cgc agg ccg cgt ccg acc gga ccg atc gtc     1512
Pro Ala Ser Arg Asp Leu Arg Arg Pro Arg Pro Thr Gly Pro Ile Val
260                 265                 270                 275

gat ggc cat gtg ctg ccg cag acc gac agc gcg gcg atc gcg gcg ggg     1560
Asp Gly His Val Leu Pro Gln Thr Asp Ser Ala Ala Ile Ala Ala Gly
                280                 285                 290

cag ctg gcg ccg gtt cgg gtc ctg atc gga acc aat gcc gac gaa ggc     1608
Gln Leu Ala Pro Val Arg Val Leu Ile Gly Thr Asn Ala Asp Glu Gly
            295                 300                 305
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cgc gcc ttc ctc ggg cgc gcg ccg atg gag acg cca gcg gac tac caa      1656
Arg Ala Phe Leu Gly Arg Ala Pro Met Glu Thr Pro Ala Asp Tyr Gln
        310                 315                 320

gcc tat ctg gag gcg cag ttt ggc gac caa gcc gcc gcc gtg gcg gcg      1704
Ala Tyr Leu Glu Ala Gln Phe Gly Asp Gln Ala Ala Ala Val Ala Ala
    325                 330                 335

tgc tat ccc ctc gac ggc cgg gcc acg ccc aag gaa atg gtc gcg cgc      1752
Cys Tyr Pro Leu Asp Gly Arg Ala Thr Pro Lys Glu Met Val Ala Arg
340                 345                 350                 355

atc ttc ggc gac aat cag ttc aat cgg ggg gtc tcg gcc ttc tcg gaa      1800
Ile Phe Gly Asp Asn Gln Phe Asn Arg Gly Val Ser Ala Phe Ser Glu
                360                 365                 370

gcg ctt gtg cgc cag ggc gcg ccc gtg tgg cgt tat cag ttc aac ggt      1848
Ala Leu Val Arg Gln Gly Ala Pro Val Trp Arg Tyr Gln Phe Asn Gly
            375                 380                 385

aat acc gag ggt gga aga gcg ccg gct acc cac gga gcc gaa att ccc      1896
Asn Thr Glu Gly Gly Arg Ala Pro Ala Thr His Gly Ala Glu Ile Pro
        390                 395                 400

tac gtt ttc ggg gtg ttc aag ctc gac gag tgg ggt ctg ttc gat tgg      1944
Tyr Val Phe Gly Val Phe Lys Leu Asp Glu Leu Gly Leu Phe Asp Trp
    405                 410                 415

ccg ccc gag ggg ccc acg ccc gcc gac cgt gcg ctg ggc caa ctg atg      1992
Pro Pro Glu Gly Pro Thr Pro Ala Asp Arg Ala Leu Gly Gln Leu Met
420                 425                 430                 435

tcc tcc gcc tgg gtc cgg ttc gcc aag aat ggc gac ccc gcc ggg gac      2040
Ser Ser Ala Trp Val Arg Phe Ala Lys Asn Gly Asp Pro Ala Gly Asp
                440                 445                 450

gcc ctt acc tgg cct gcc tat tct acg ggc aag tcg acc atg aca ttc      2088
Ala Leu Thr Trp Pro Ala Tyr Ser Thr Gly Lys Ser Thr Met Thr Phe
            455                 460                 465

ggt ccc gag ggc cgc gcg gcg gtg gtg tcg ccc gga cct tcc atc ccc      2136
Gly Pro Glu Gly Arg Ala Ala Val Val Ser Pro Gly Pro Ser Ile Pro
        470                 475                 480

cct tgc gcg gat ggc ggc aag gcg ggg ggc gga ggc agc ggc gga ggc      2184
Pro Cys Ala Asp Gly Ala Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly
    485                 490                 495

agc ggc gga ggc agc aaa gac aac gtt gcg gac gtg gta gtg gtg ggc      2232
Ser Gly Gly Gly Ser Lys Asp Asn Val Ala Asp Val Val Val Val Gly
500                 505                 510                 515

gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc cag gcc gcc ggt      2280
Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly
                520                 525                 530

ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta ggg gga aag act      2328
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Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr
            535                 540                 545

ctg agc gta caa tcg ggt ccc ggc agg acg act atc aac gac ctc ggc      2376
Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly
        550                 555                 560

gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc agg ttg ttt      2424
Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe
    565                 570                 575

gaa aga ttt cat ttg gag ggc gag ctc cag agg acg act ggg aat tca      2472
Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser
580                 585                 590

atc cat caa gca caa gac ggt aca acc act aca act gct cct tat ggt gac      2520
Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp
            600                 605                 610

tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg gaa ctc ctc ccc      2568
Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro
        615                 620                 625

gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac ctc aag gcg      2616
Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala
    630                 635                 640

agc cct cag gcg aag cgg ctc gac agt gtg agc ttc gcg cac tac tgt      2664
Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys
645                 650                 655

gag aag gaa cta aac ttg cct gct gtt ctc ggc gta gca aac cag atc      2712
Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile
660                 665                 670                 675

aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc agc atg ctt ttt      2760
Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu Phe
            680                 685                 690

ctc acc gac tac atc aag agt gcc acc ggt ctc agt aat atc ttc tcg      2808
Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser
        695                 700                 705

gac aag aaa gac ggc ggg cag tat atg cga tgc aaa acg ggt atg cag      2856
Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln
    710                 715                 720

tcg att tgc cat gcc atg tca aag gaa ctt gtt cca ggc tca gtg cac      2904
Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His
725                 730                 735

ctc aac acc ccc gtc gct gaa att gag cag tcg gca tcc ggc tgt acg      2952
Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr
740                 745                 750                 755

gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt      3000
Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val Val
```

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                    760                 765                 770

tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt tca cca cct ctt  3048
Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu
                775                 780                 785

ccc gcc gag aag caa gca ttg gcg gaa aat tct atc ctg ggc tac tat  3096
Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr
            790                 795                 800

agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc gaa caa ggc  3144
Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly
        805                 810                 815

ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc tca ttt gcc aga  3192
Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg
    820                 825                 830

gat acc agc atc gac gtc gat cga caa tgg tcc att acc tgt ttc atg  3240
Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met
835                 840                 845

gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc aag cag gta cga  3288
Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg
            850                 855                 860

caa aag tct gtc tgg gac caa ctc cgc gca gcc tac gag aac gcc ggg  3336
Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly
        865                 870                 875

gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc gag tgg tcg aag  3384
Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys
    880                 885                 890

cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg ctg aac gat  3432
Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp
895                 900                 905

ctc atc aca ctg ggt tcg gcg ctc agg acg ccg ttc aag agt gtt cat  3480
Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His
            910                 915                 920

ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat atg gaa ggg  3528
Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly
        925                 930                 935

gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt gtg gct agc ctg  3576
Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu
    940                 945                 950

gtg cca gca gca tag                                             3591
Val Pro Ala Ala
955

<210>  31
<211>  1196
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<213> PRT
<214> Unknown

<220>
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<223> gst + polylinker

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<222> (2164)..(2199)
<223> spacer sequence

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<222> (2200)..(3558)
<223> K::trAPAO

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<222> (2200)..(2202)
<223> extra lysine

<400> 31

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln
-225 -220 -215

Pro Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu
-210 -205 -200

His Leu Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys
-195 -190 -185

Phe Glu Leu Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp
-180 -175 -170

Gly Asp Val Lys Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile
-165 -160 -155

Ala Asp Lys His Asn Met Leu Gly Gly Cys Pro Lys Glu Arg Ala
-150 -145 -140

Glu Ile Ser Met Leu Glu Gly Ala Val Leu Asp Ile Arg Tyr Gly
-135 -130 -125

Val Ser Arg Ile Ala Tyr Ser Lys Asp Phe Glu Thr Leu Lys Val

-120 -115 -110

Asp Phe Leu Ser Lys Leu Pro Glu Met Leu Lys Met Phe Glu Asp Arg
-105 -100 -95

Leu Cys His Lys Thr Tyr Leu Asn Gly Asp His Val Thr His Pro Asp
-90 -85 -80

Phe Met Leu Tyr Asp Ala Leu Asp Val Val Leu Tyr Met Asp Pro Met
-75 -70 -65

Cys Leu Asp Ala Phe Pro Lys Leu Val Cys Phe Lys Lys Arg Ile Glu
-60 -55 -50

Ala Ile Pro Gln Ile Asp Lys Tyr Leu Lys Ser Ser Lys Tyr Ile Ala
-45 -40 -35 -30

Trp Pro Leu Gln Gly Trp Gln Ala Thr Phe Gly Gly Gly Asp His Pro
-25 -20 -15

Pro Lys Ser Asp Leu Val Pro Arg Gly Ser Pro Glu Phe Thr Asp Phe
-10 -5 -1 1

Pro Val Arg Arg Thr Asp Leu Gly Gln Val Gln Gly Leu Ala Gly Asp
5 10 15

Val Met Ser Phe Arg Gly Ile Pro Tyr Ala Ala Pro Pro Val Gly Gly
20 25 30 35

Leu Arg Trp Lys Pro Pro Gln His Ala Arg Pro Trp Ala Gly Val Arg
40 45 50

Pro Ala Thr Gln Phe Gly Ser Asp Cys Phe Gly Ala Ala Tyr Leu Arg
55 60 65

Lys Gly Ser Leu Ala Pro Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn
70 75 80

Val Trp Ala Pro Ser Gly Ala Lys Pro Gly Gln Tyr Pro Val Met Val
85 90 95

Trp Val Tyr Gly Gly Gly Phe Ala Gly Gly Thr Ala Ala Met Pro Tyr
100 105 110 115

Tyr Asp Gly Glu Ala Leu Ala Arg Gln Gly Val Val Val Val Thr Phe
120 125 130

Asn Tyr Arg Thr Asn Ile Leu Gly Phe Phe Ala His Pro Gly Leu Ser
135 140 145

Arg Glu Ser Pro Thr Gly Thr Ser Gly Asn Tyr Gly Leu Leu Asp Ile
150 155 160

Leu Ala Ala Leu Arg Trp Val Gln Ser Asn Ala Arg Ala Phe Gly Gly
165 170 175

Asp Pro Gly Arg Val Thr Val Phe Gly Glu Ser Ala Gly Ala Ser Ala
180 185 190 195

Ile Gly Leu Leu Leu Thr Ser Pro Leu Ser Lys Gly Leu Phe Arg Gly
200 205 210

Ala Ile Leu Glu Ser Pro Gly Leu Thr Arg Pro Leu Ala Thr Leu Ala
215 220 225

Asp Ser Ala Ala Ser Gly Glu Arg Leu Asp Ala Asp Leu Ser Arg Leu
230 235 240

Arg Ser Thr Asp Pro Ala Thr Leu Met Ala Arg Ala Asp Ala Ala Arg
245 250 255

Pro Ala Ser Arg Asp Leu Arg Arg Pro Arg Pro Thr Gly Pro Ile Val
260 265 270 275

Asp Gly His Val Leu Pro Gln Thr Asp Ser Ala Ala Ile Ala Ala Gly
280 285 290

Gln Leu Ala Pro Val Arg Val Leu Ile Gly Thr Asn Ala Asp Glu Gly
295 300 305

Arg Ala Phe Leu Gly Arg Ala Pro Met Glu Thr Pro Ala Asp Tyr Gln
310 315 320

Ala Tyr Leu Glu Ala Gln Phe Gly Asp Gln Ala Ala Ala Val Ala Ala
325 330 335

Cys Tyr Pro Leu Asp Gly Arg Ala Thr Pro Lys Glu Met Val Ala Arg
340 345 350 355

Ile Phe Gly Asp Asn Gln Phe Asn Arg Gly Val Ser Ala Phe Ser Glu
360 365 370

Ala Leu Val Arg Gln Gly Ala Pro Val Trp Arg Tyr Gln Phe Asn Gly
375 380 385

Asn Thr Glu Gly Gly Arg Ala Pro Ala Thr His Gly Ala Glu Ile Pro
390 395 400

Tyr Val Phe Gly Val Phe Lys Leu Asp Glu Leu Gly Leu Phe Asp Trp
405 410 415

Pro Pro Glu Gly Pro Thr Pro Ala Asp Arg Ala Leu Gly Gln Leu Met
420 425 430 435

Ser Ser Ala Trp Val Arg Phe Ala Lys Asn Gly Asp Pro Ala Gly Asp
440 445 450

Ala Leu Thr Trp Pro Ala Tyr Ser Thr Gly Lys Ser Thr Met Thr Phe
455 460 465

Gly Pro Glu Gly Arg Ala Ala Val Val Ser Pro Gly Pro Ser Ile Pro
470 475 480

Pro Cys Ala Asp Gly Ala Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly
485 490 495

Ser Gly Gly Gly Ser Lys Asp Asn Val Ala Asp Val Val Val Val Gly
500 505 510 515

Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly
520 525 530

Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr
535 540 545

Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly
550 555 560

Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe
565 570 575

Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser
580 585 590 595

Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp
600 605 610

Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro
615 620 625

Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala
630 635 640

Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys
645 650 655

Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile
660 665 670 675

Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu Phe
680 685 690

Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser
695 700 705

Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln
710 715 720

Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His
725 730 735

Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr
740 745 750 755

Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val Val
760 765 770

Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu
775 780 785

Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr

790 795 800

Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly
805 810 815

Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg
820 825 830 835

Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met
840 845 850

Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg
855 860 865

Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly
870 875 880

Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys
885 890 895

Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp
900 905 910 915

Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His
920 925 930

Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly
935 940 945

Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu
950 955 960

Val Pro Ala Ala
965

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<211> 1803
<212> DNA
<213> Unknown

<220>
<223> Glyc(-) mutation in glycosylation sites (Exophiala spinifera)

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<221> CDS

<220> (1)..(1803)
<223>

<400> 32

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atg gca ctt gca ccg agc tac atc aat ccc cca aac gtc gcc tcc cca      48
Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro
1               5                  10                  15

gca ggg tat tct cac gtc ggc gta ggc cca gac gga ggg agg tat gtg      96
Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val
            20                  25                  30

aca ata gct gga cag att gga caa gac gct tcg ggc gtg aca gac cct     144
Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro
        35                  40                  45

gcc tac gag aaa cag gtt gcc caa gca ttc gcc aat ctg cga gct tgc     192
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
    50                  55                  60

ctt gct gca gtt gga gcc act tca aac gac gtc acc aag ctc aat tac     240
Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr
65                  70                  75                  80

tac atc gtc gac tac gcc ccg agc aaa ctt acc gca att gga gat ggg     288
Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
                85                  90                  95

ctg aag gct acc ttt gcc ctt gac agg ctc cct cct tgc acg ctg gtg     336
Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
            100                 105                 110

cca gtg tcg gcc ttg tct tca cct gaa tac ctc ttt gag gtt gat gcc     384
Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
        115                 120                 125

acg gcg ctg gtg ccg gga cac acg acc cca gac aac gtt gcg gac gtg     432
Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val
    130                 135                 140

gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc     480
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
145                 150                 155                 160

cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta     528
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
                165                 170                 175

ggg gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg act atc     576
Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile
            180                 185                 190

aac gac ctc ggc gct gcg tgg atc aat gat agc aat cag gcc gaa gta     624
Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ala Glu Val
        195                 200                 205

tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg     672
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Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr
    210                 215                 220

act gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct  720
Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala
225                 230                 235                 240

cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gtg  768
Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala
                245                 250                 255

gaa ctt ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa  816
Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln
            260                 265                 270

gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc  864
Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe
        275                 280                 285

gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta  912
Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val
    290                 295                 300

gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc  960
Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile
305                 310                 315                 320

agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt 1008
Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser
                325                 330                 335

aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa 1056
Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys
            340                 345                 350

aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca 1104
Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro
        355                 360                 365

ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca 1152
Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala
    370                 375                 380

tcc ggc tgt acg gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa 1200
Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys
385                 390                 395                 400

aag gtg gtg gtt tcg tta ccg acg acc ttg tat ccc acc ttg acg ttt 1248
Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe
                405                 410                 415

tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc 1296
Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile
            420                 425                 430

ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg 1344
Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp
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        435                 440                 445

cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc      1392
Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile
    450                 455                 460

tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att      1440
Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile
465                 470                 475                 480

acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc      1488
Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser
                485                 490                 495

aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac      1536
Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr
            500                 505                 510

gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc      1584
Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile
        515                 520                 525

gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat      1632
Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr
    530                 535                 540

ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc      1680
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe
545                 550                 555                 560

aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg      1728
Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly
                565                 570                 575

tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt      1776
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val
            580                 585                 590

gtg gct agc ctg gtg cca gca gca tag                                 1803
Val Ala Ser Leu Val Pro Ala Ala
        595                 600
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<212> PRT
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<223> Glyc(-) APAO; mutation in glycosylation sites (Exophiala spinifera)

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1               5                   10                  15
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Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro
35 40 45

Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
50 55 60

Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr
65 70 75 80

Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
85 90 95

Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
100 105 110

Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
115 120 125

Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val
130 135 140

Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
145 150 155 160

Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
165 170 175

Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile
180 185 190

Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ala Glu Val
195 200 205

Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr
210 215 220

Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala
225 230 235 240

Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala

245 250 255

Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln
260 265 270

Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe
275 280 285

Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val
290 295 300

Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile
305 310 315 320

Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser
325 330 335

Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys
340 345 350

Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro
355 360 365

Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala
370 375 380

Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys
385 390 395 400

Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe
405 410 415

Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile
420 425 430

Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp
435 440 445

Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile
450 455 460

Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile
465 470 475 480

Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser
485 490 495

Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr
500 505 510

Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile
515 520 525

Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr
530 535 540

Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe
545 550 555 560

Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly
565 570 575

Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val
580 585 590

Val Ala Ser Leu Val Pro Ala Ala
595 600

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<213> Artificial Sequence

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<400> 34
ggggaattca tggcacttgc accgagctac atcaatc 37

<210> 35
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<212> DNA
<213> Exophiala spinifera

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<222> (1134)..(1186)
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<400> 35
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caacatcggcg taggccctaa cgaagcgagg tatgtgacaa tagctggaca gattggacaa 120

gacgctttgg gcgtgacaga cccagcctac gagaaacagg ttgcccaagc attcgccaat 180

ctacgagctt gccttgctgc agttggagcc tcttcaaacg acgtcacccaa gctcaattac 240

tacatcgtcg actacgcccc gagcaaactc accgcaattg gagatgggct gaagtctacc 300

tttgccctg acaggctccc tccttgcacg ctggtgccag tacccgcctt ggctttcacct 360

gaatacctct ttgaggttga tgccacggcg ctggtgccag gacactcgac cccagacaac 420

gttgcggacg tggtagtggt gggcgctggc ttgagcggtt tggagacggc acgcaaagtc 480

caggccgccg gtctgtcctg cctcgttctt gaggcgatgg atcgtgtagg gggaaagact 540

ctgagcgtac aatcgggtcc cggcaggacg actatcaacg accttgggcgc tgcgtggatc 600

aatgacagca accaaagcga agtatccaga ttgtttgaaa gatttcattt ggagggcgag 660

ctccagagga cgaccggaaa ttcaatccat caagcacaag acggtacaac cactacagct 720

cctatggtg actccccggt aagcacaatc ccactttgtg atgagacctc tgtcgagtgt 780

agaatacagt cactgactcc acttcgtcca gctgagcgag gaggttgcaa gtgcacttgc 840

ggaactcctc ccccgtatggt ctcagctgat cgaagagtat agccttgaag accccaaggc 900

gagccctcag gcgaagcggc tcgacagtgt gagcttcgcg cactactgtg agaaggacct 960

aaacttgcct gctgttctca gcgtggcaaa ccagatcaca cgcgctctgc tcggtgtgga 1020

agcccacgag atcagcatgc ttttttctac cgactacatc aagagtgcca ccggtctcag 1080

taatattgtc tcggacaaga aagacggcgg gcagtatatg cgatgcaaaa caggtgcgtg 1140

cggtgtcctc tcaggtaggg gactcgtttc ttagtggtca ttccaggtat gcagtcgatt 1200

tgccatgcca tgtcaaagga acttgttcca ggctcagtgc acctcaacac ccccgtcgct 1260

ggaattgagc agtcggcgtc cggctgtata gtacgatcgg cctcgggcgc cgtgttccga 1320

agcaaaaagg tggtggtttc gttaccgaca acattgtatc ccaccttgac attttcacca 1380

cctcttcccg ccgagaagca agcattggcg gaaaaatcta tcctcggcta ctatagcaag 1440

atagtcttcg tatgggacaa ccccgtggtgg cgcgaacaag gcttctcggg cgtcctccaa 1500

tcgagctgtg acccccatct atttgccaga gataccagca tcgaagtcga tcggcaatgg 1560

tccattacct gtttcatggt cggagacccg ggacggaagt ggtcccaaca gtccaagcag 1620

gtacgacaaa agtctgtctg ggaccaactc cgcgcagcct acgagaacgc cgggcccaa 1680

gtcccagagc cggccaacgt gctcgaaatc gagtggtcga agcagcagta tttccaagga 1740

gctccgagcg ccgtctatgg gctgaacgat ctcatcacac tgggttcggc gctcagaacg 1800

ccgttcaagt gtgttcattt cgttggaacg gagacgtctt tagtttggaa agggtatatg 1860

gaagggccca tacgatcggg tcaacgaggt gctgcagaag ttgtggctag cctggtgcca 1920

gtagcatag 1929

<210> 36
<211> 600
<212> PRT
<213> Exophilia spinifera

<400> 36

Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro
1 5 10 15

Ala Gly Tyr Ser His Ile Gly Val Gly Pro Asn Glu Ala Arg Tyr Val
20 25 30

Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Leu Gly Val Thr Asp Pro
35 40 45

Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
50 55 60

Leu Ala Ala Val Gly Ala Ser Ser Asn Asp Val Thr Lys Leu Asn Tyr
65 70 75 80

Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
85 90 95

Leu Lys Ser Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
100 105 110

Pro Val Pro Ala Leu Ala Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
115 120 125

Thr Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val
130 135 140

Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
145 150 155 160

Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
165 170 175

Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile
180 185 190

Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val
195 200 205

Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr
210 215 220

Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala
225 230 235 240

Pro Tyr Gly Asp Ser Pro Leu Ser Glu Glu Val Ala Ser Ala Leu Ala
245 250 255

Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu Tyr Ser Leu Glu
260 265 270

Asp Pro Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe
275 280 285

Ala His Tyr Cys Glu Lys Asp Leu Asn Leu Pro Ala Val Leu Ser Val
290 295 300

Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile
305 310 315 320

Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser
325 330 335

Asn Ile Val Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys
340 345 350

Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro
355 360 365

Gly Ser Val His Leu Asn Thr Pro Val Ala Gly Ile Glu Gln Ser Ala
370 375 380

Ser Gly Cys Ile Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys
385 390 395 400

Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe
405 410 415

Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Lys Ser Ile
420 425 430

Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Asn Pro Trp Trp
435 440 445

Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile
450 455 460

Ser Phe Ala Arg Asp Thr Ser Ile Glu Val Asp Arg Gln Trp Ser Ile
465 470 475 480

Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser
485 490 495

Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr
500 505 510

Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile
515 520 525

Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr
530 535 540

Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe
545 550 555 560

Lys Cys Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly
565 570 575

Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val
580 585 590

Val Ala Ser Leu Val Pro Ala Ala

595 600

<210> 37
<211> 1929
<212> DNA
<213> Exophiala spinifera

<220>
<221> Intron
<222> (789)..(811)
<223>

<220>
<221> Intron
<222> (1134)..(1186)
<223>

<400> 37
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gagcctttgc gcgtgacaga cccagcctac gagaaacagg ttgcccaagc attcgccaat 180

ctgcgagctt gccttgctgc agttggagcc tcttcaaacg acgtcaccaa gctcaattac 240

tacatcgtcg actacgcccc gagcaaactc accgcaattg gagatgggct gaagtctacc 300

tttgcccttg acaggctccc tccttgcacg ctggtgccag taccggcctt ggcttcacct 360

gaatacctct ttgaggttga cgccacggcg ctggtgccag gacactcgac cccagacaac 420

gttgcggacg tggtagtggt gggcgctggc ttgagcggct tggagacggc acgcaaagtc 480

caggccgccg gtctgtcctg cctcgttctt gaggcgatgg atcgtgtagg gggaaagact 540

ctgagcgtac aatcgggtcc cggcaggacg actatcaacg acctcggcgc tgcgtggatc 600

aatgacagca accaaagcga agtatccaga ttgtttgaaa gatttcattt ggagggcgag 660

ctccagagga cgaccggaaa ttcaatccat caagcacaag acggtacaac cactacagct 720

cctatggtg actccccggt aagcacaatc ccactttgtg atgagacctc tgtcgagtgt 780

agaatacagt cactgactcc acttcgtcca gctgagcgag gaggttgcaa gtgcacttgc 840

ggaactcctc ccgtatggt ctcagctgat cgaagagtat agccttgaag accccaaggc 900

gagcctcag gcgaagcggc tcgacagtgt gagcttcgcg cactactgtg agaaggacct 960

aaacttgcct gctgttctca gcgtggcaaa ccagatcaca cgcgctctgc tcggtgtgga 1020

agcccacgag atcagcatgc ttttttctac cgactacatc aagagtgcca ccggtctcag 1080

taatattgtc tcggacaaga aagacggcgg gcagtatatg cgatgcaaaa caggtgcgtg 1140

cggtgtcctc tcaggtaggg gactcgtttc ttagtggtca ttccaggtat gcagtcgatt 1200

tgccatgcca tgtcaaagga acttgttcca ggctcagtgc acctcaacac ccccgtcgct 1260

gtaaattgag agtcgggcgt cggctgtata gtacgatcgg cctcgggcgc cgtgttccga 1320

atcaaaaagg tggtggtttc gttaccgaca acattgtatc ccaccttgac attttcacca 1380

cctcttcccg ccgagaagca agcattgggg gaaaaatcta tcctcggcta ctatagcaag 1440

atagtcttcg tatgggacaa cccgtggtgg cgcgaacaag gcttctcggg cgtccttcaa 1500

tcgagctgtg accccatctc atttgccaga gatacgagca tcgaagtcga tcggcaatgg 1560

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ctgttcaagt gtgttcattt cgttggaacg gagacgtctt tagtttggaa agggtatatg 1860

taagtggccc tacgatcggg tcaacgaggt gctgcagaag ttgtggctag cctggtgcca 1920

tcagcatag 1929

<210> 38
<211> 600
<212> PRT
<213> Exophiala spinifera

<400> 38

Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro
1 5 10 15

Ala Gly Tyr Ser His Ile Gly Val Gly Pro Asn Glu Ala Arg Tyr Val
20 25 30

Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Leu Gly Val Thr Asp Pro
35 40 45

Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
50 55 60

Leu Ala Ala Val Gly Ala Ser Ser Asn Asp Val Thr Lys Leu Asn Tyr
65 70 75 80

Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly

85 90 95

Leu Lys Ser Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
100 105 110

Pro Val Pro Ala Leu Ala Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
115 120 125

Thr Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val
130 135 140

Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
145 150 155 160

Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
165 170 175

Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile
180 185 190

Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val
195 200 205

Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr
210 215 220

Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala
225 230 235 240

Pro Tyr Gly Asp Ser Pro Leu Ser Glu Glu Val Ala Ser Ala Leu Ala
245 250 255

Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu Tyr Ser Leu Glu
260 265 270

Asp Pro Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe
275 280 285

Ala His Tyr Cys Glu Lys Asp Leu Asn Leu Pro Ala Val Leu Ser Val
290 295 300

Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile
305 310 315 320

Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser
325 330 335

Asn Ile Val Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys
340 345 350

Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro
355 360 365

Gly Ser Val His Leu Asn Thr Pro Val Ala Gly Ile Glu Gln Ser Ala
370 375 380

Ser Gly Cys Ile Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys
385 390 395 400

Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe
405 410 415

Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Lys Ser Ile
420 425 430

Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Asn Pro Trp Trp
435 440 445

Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile
450 455 460

Ser Phe Ala Arg Asp Thr Ser Ile Glu Val Asp Arg Gln Trp Ser Ile
465 470 475 480

Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser
485 490 495

Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr
500 505 510

Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile
515 520 525

Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr
530 535 540

Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe
545 550 555 560

Lys Cys Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly
565 570 575

Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val
580 585 590

Val Ala Ser Leu Val Pro Ala Ala
595 600

<210> 39
<211> 1930
<212> DNA
<213> Exophiala spinifera

<220>
<221> Intron
<222> (739)..(811)
<223>

<220>
<221> Intron
<222> (1134)..(1187)
<223>

<220>
<221> misc_feature
<222> (649)..(649)
<223> n = A,T,C or G

<400> 39
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cacgtcggcg taggcccaga cggagggagg tatgtgacaa tagctggaca gattggacaa 120

gacgcttcgg gcgtgacaga ccctgcctac gagaaacagg ttgcccaagc attcgccaat 180

ctgcgagctt gccttgctgc agttggagcc acttcaaacg acgtcaccaa gctcaattac 240

tacatcgtcg actacgcccc gagcaaactc accgcaattg gagatgggct gaaggctacc 300

tttgcccttg acaggctccc tccttgcacg ctggtgccag tgtcggcctt gtcttcacct 360

gaatacctct ttgaggttga tgccacggcg ctggtgccgg gacacacgac cccagacaac 420

gttgcggacg tggtagtggt gggcgctggc ttgagcggtt tggagacggc acgcaaagtc 480

caggccgccg gtctgtcctg cctcgttctt gaggcgatgg atcgtgtagg gggaaagact 540

ctgagcgtac aatcgggtcc cggcaggacg actatcaacg acctcggcgc tgcgtggatc 600

aatgacagca acccaaagcga agtatccaga ttgtttgaaa gatttcatnt ggagggcgag 660

ctccagagga cgactggaaa ttcaatccat caagcacaag acggtacaac cactacagct 720

cctatggtg actccttggt aagcacaatc ccactttgtg atgagacctc tgtcgagtgt 780

agaatacagt cactgattcc acttcgtcca gctgagcgag gaggttgcaa gtgcacttgc 840

ggaactcctc cccgtatggt ctcagctgat cgaagagcat agccttcaag acctcaaggc 900

gagccctcag gcgaaggcggc tcgacagtgt gagcttcgcg cactactgtg agaaggaact 960

aaacttgcct gctgttctcg gcgtagcaaa ccagatcaca cgcgctctgc tcggtgtgga 1020

agccacgag atcagcatgc ttttttctac cgactacatc aagagtgcca ccggtctcag 1080

taatattttc tcggacaaga aagacggcgg gcagtatatg cgatgcaaaa caggtgcgtg 1140

tggtgtcgtc tcaggtgggg gactcgtttc tcaagtggtc atttcaggta tgcagtcgat 1200

ttgccatgcc atgtcaaagg aacttgttcc aggctcagtg cacctcaaca ccccgtcgc 1260

tgaaattgag cagtcggcat ccggctgtac agtacgatcg gcctcgggcg ccgtgttccg 1320

aagcaaaaag gtggtggttt cgttaccgac aaccttgtat cccaccttga catttttcacc 1380

accctccccc gccgagaagc aagcattggc ggaaaattct atcctgggct actatagcaa 1440

gatagtcttc gtatgggaca agccgtggtg gcgcgaacaa ggcttctcgg gcgtcctcca 1500

atcgagctgt gaccccatct catttgccag agataccagc atcgacgtcg atcgacaatg 1560

gtccattacc tgtttcatgg tcggagaccc gggacggaag tggtcccaac agtccaagca 1620

ggtacgacaa aagtctgtct gggaccaact ccgcgcagcc tacgagaacg ccgggcccca 1680

agtcccagag ccggccaacg tgctcgaaat cgagtggtcg aagcagcagt atttccaagg 1740

agctccgagc gccgtctatg ggctgaacga tctcatcaca ctgggttcgg cgctcagaac 1800

gccgttcaag agtgttcatt tcgttggaac ggagacgtct ttagtttgga aagggtatat 1860

ggaaggggcc atacgatcgg gtcaacgagg tgctgcagaa gttgtggcta gcctggtgcc 1920

agcagcatag 1930

<210> 40
<211> 598
<212> PRT
<213> Exophiala spinifera

<220>
<221> MISC_FEATURE
<222> (216)..(216)

<223> Xaa = any amino acid

<400> 40

Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro
1 5 10 15

Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val
20 25 30

Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro
35 40 45

Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
50 55 60

Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr
65 70 75 80

Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
85 90 95

Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
100 105 110

Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
115 120 125

Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val
130 135 140

Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln
145 150 155 160

Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly
165 170 175

Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn
180 185 190

Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser
195 200 205

Arg Leu Phe Glu Arg Phe His Xaa Glu Gly Glu Leu Gln Arg Thr Thr
210 215 220

Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro
225 230 235 240

Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu
245 250 255

Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp
260 265 270

Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala
275 280 285

His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Asn
290 295 300

Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met
305 310 315 320

Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile
325 330 335

Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly
340 345 350

Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser
355 360 365

Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly
370 375 380

Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val
385 390 395 400

Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro
405 410 415

Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly
420 425 430

Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu

435 440 445

Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe
450 455 460

Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys
465 470 475 480

Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln
485 490 495

Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn
500 505 510

Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp
515 520 525

Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu
530 535 540

Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser
545 550 555 560

Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met
565 570 575

Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala
580 585 590

Ser Leu Val Pro Ala Ala
595

<210> 41
<211> 1928
<212> DNA
<213> Rhinocladiella atrovirens

<220>
<221> Intron
<222> (739)..(811)
<223>

<220>
<221> Intron
<222> (1134)..(1185)
<223>

<400> 41
atggcacttg cacgagcta catcaatccc ccaaacctcg cctcccagc agggtattcc 60

cacgtcggcg taggcccaaa cggagggagg tatgcgacaa tagctggaca gattggacaa 120

gacgcttcgg ccgtgacaga ccctgcctac gagaaacagg ttgcccaagc attcgccaac 180

ctgcgagctt gtcttgctgc agttggagcc actccaaacg acattaccaa gctcaattac 240

tacatcgtcg actacaaccc gagcaaactc accgcaattg gagatgggct gaaggctacc 300

tttgcccttg acaggctccc tccttgcacg ctggtgccag tgcccgccct ggcttcacct 360

gaatacccct ttgaggttga tgccacgggc gtggttccag gacactcaac cccagacaat 420

gttgcggacg tggtcgtggt gggcgctggc ttgagcggct tggagacggc acgcaaagtc 480

caggctgccg ggctgtcctg cctcgttctt gaggcgatgg atgtgtgggg gggaaagact 540

ctgagcgtac aatcgggtcc cggcaggacg gctatcaatg acctcggcgc tgcgtggatc 600

aatgacagca accaaagcga agtattcaaa ttatttgaaa gatttcattt ggagggcgag 660

ctccagagga cgaccggaaa ttcaatccat caagcacaag acggtacaac cactacagct 720

cctatgggtg attcctggct aagcacaatt ccatcttgtg atgagacctc tgtcgtgtgt 780

agaatacagt cgctgactcc acatcgtcca gctgaggcgag gaggttgcaa gtgcactcgc 840

ggaactcctt ccccatggtt ctcagctgat cgaagagcat agtcttgaag accccaaggc 900

gagcctcaa gcgaagcagc tcgacagtgt gagcttcgca cactactgtg agaaggatct 960

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tggtgttctc tcagtgggag actcgtttct tagtggtcat tccaggtatg cagtcgcttt 1200

gccatgccat gtcaaaggaa cttgttccag gctcagtgca cctcaacacc ccccgtcgccg 1260

aaattgagca gtcggcatcc ggctgtacag tacgatcggc ctcgggcggc gtgttccgaa 1320

gtaaaaaggt ggtggtttcg ttacccgacaa ccttgtatcc cacccttgata ttttcaccac 1380

ctcttccccc cgagaagcaa gcattggctg aaaaatccat cctgggctac tatagcaaga 1440

tagtcttcgt atgggacaag ccgtggtggc gcgaacaagg cttctcgggc gtcctccaat 1500

cgagctgtga ccccatctca tttgccagag ataccagcat cgaagtcgat cggcaatggt 1560

ccattacctg tttcatggtc ggagaccccg gacggaagtg gtcccaacag tccaagcagg 1620

tacgacagaa gtctgtctgg aaccaactcc gcgcagccta cgagaacgcc gggggccaag 1680

tccagagccc ggccaacgtg ctcgagatcg agtggtcgaa gcagcagtat ttccaaggag 1740

cgccgagcgt cgtctatggg ctgaactgtc tcaacacact gggttcggcg ctcagaacgc 1800

cgttcaaggg tgttcatttc gttcggaacgg agacgtcttt ggtttggaaa gggtatatgg 1860

aaggggccat acgatcgggt cagcgaggcg ctgcagaagt tgtggctagc ctggtgccag 1920

ctgcatag 1928

<210> 42
<211> 538
<212> PRT
<213> Rhinocladiella atrovirens

<400> 42

Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Leu Ala Ser Pro
1 5 10 15

Ala Gly Tyr Ser His Val Gly Val Gly Pro Asn Gly Gly Arg Tyr Ala
20 25 30

Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Ala Val Thr Asp Pro
35 40 45

Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
50 55 60

Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Ile Thr Lys Leu Asn Tyr
65 70 75 80

Tyr Ile Val Asp Tyr Asn Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
85 90 95

Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
100 105 110

Pro Val Pro Ala Leu Ala Ser Pro Glu Tyr Pro Phe Glu Val Asp Ala
115 120 125

Thr Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val
130 135 140

Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
145 150 155 160

Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
165 170 175

Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Ala Ile
180 185 190

Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val
195 200 205

Phe Lys Leu Phe Glu Arg Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly
210 215 220

Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr
225 230 235 240

Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu
245 250 255

Leu Pro Ala Trp Ser Gln Leu Ile Glu Glu His Ser Leu Glu Asp Pro
260 265 270

Lys Ala Ser Pro Gln Ala Lys Gln Leu Asp Ser Val Ser Phe Ala His
275 280 285

Tyr Cys Glu Lys Asp Leu Ser Leu Pro Ala Val Leu Gly Val Ala Asn
290 295 300

Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met
305 310 315 320

Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile
325 330 335

Val Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly
340 345 350

Met Gln Ser Leu Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser
355 360 365

Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly
370 375 380

Cys Thr Val Arg Ser Ala Ser Gly Gly Val Phe Arg Ser Lys Lys Val
385 390 395 400

Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Ile Phe Ser Pro
405 410 415

Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Lys Ser Ile Leu Gly
420 425 430

Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu
435 440 445

Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe
450 455 460

Ala Arg Asp Thr Ser Ile Glu Val Asp Arg Gln Trp Ser Ile Thr Cys
465 470 475 480

Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln
485 490 495

Val Arg Gln Lys Ser Val Trp Asn Gln Leu Arg Ala Ala Tyr Glu Asn
500 505 510

Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp
515 520 525

Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Val Val Tyr Gly Leu
530 535 540

Asn Cys Leu Asn Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Gly
545 550 555 560

Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met
565 570 575

Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala
580 585 590

Ser Leu Val Pro Ala Ala
595

<213> 43
<211> 1928
<212> DNA
<213> Rhinocladiella atrovirens

<220>
<221> Intron
<222> (739)..(811)
<223>

<220>
<221> Intron
<222> (1134)..(1186)
<223>

<400> 43
atgtcactta cacgagctca catcaatccc ccaaacctcg cctcccagc agggtatttc 60

tcgtcggcg taggcccaaa cggagggagg tatgtgacaa tagctggaca gattggacaa 120

gacgttggg cgtgacaga ccctgcctac gagaaacagg ttgcccaagc attcgccaac 180

ctgcgagctt gtcttgctgc agttggagcc actcaaacg acattaccaa gctcaattac 240

tacatcgtcg actacaaccc gagcaaactc accgcaattg gagatgggct gaaggctacc 300

tttgccctg acaggctccc tccttgcacg ctggtgccag tgccgggcct ggcttcacct 360

gaatacctct ttgaggttga tgccacgggg ctggttccag gacactcaac cccagacaat 420

gttgcggacg tggtcgtggt gggcgctggc ttgagcgggt tggagacggc acgcaaagtc 480

caggctgccg ggctgtcctg cctcgttctt gagggcatgg atcgtgtggg gggaaagact 540

ctgaccgtac aatcgggtcc cggcaggacg actatcaatg acctcggcgc tgcgtggatc 600

aatgacagca accaaagcga agtattcaaa ttatttgaaa gatttcattt ggagggcgag 660

ctccagagga cgaccggaaa ttcaatccat caagcacaag acggtacaac cactacagct 720

ccttatgggtg attcccctggt aagcacaatt ccatcttgtg atgagacctc tgtcgtgtgt 780

agaatacagt cgctgactcc acatcgtcca gctgagcgag gaggttgcaa gtgcactcgc 840

ggaactcctt cccgcatggt ctcagctgat cgaagagcat agtcttgaag accccaaggc 900

gagccctcaa gcgaagcagc tcgacagtgt gagcttcgca cactactgtg agaaggatct 960

aaacttgcct gctgttctcg gcgtggcaaa ccagatcaca cgcgctctgc tcggtgtgga 1020

agcccacgag atcagcatgt ttttttctac cgactacatc aagagtgcca ccggtctcag 1080

taatattgtc tcggataaga aagacggtgg gcagtatatg cgatgcaaaa caggtgcgtg 1140

tggtgttctc tcagtgggag actcgtttct tagtggtcat tccaggtatg cagtcgcttt 1200

gccatgccat gtcaaaggaa cttgttccag gctcagtgca cctcaacacc cccgtcgccg 1260

aaattgagca gtcggcatcc ggctgtacag tacgatcggc ctcgggcggc gtgttccgaa 1320

gtaaaaaggt ggtggtttcg ttaccgacaa ccttgtatcc caccttgata ttttcaccac 1380

ctcttcccgc cgagaagcaa gcattggctg aaaaatccat cctgggctac tatagccaaga 1440

tagtcttcgt atgggacaag ccgtggtggc gcgaacaagg cttctcgggc gtcctccaat 1500

cgagctgtga ccccatctca tttgccagag ataccagcat cgaagtcgat cggcaatggt 1560

ccatcacctg tttcatggtc ggagaccccgg gacggaagtg gtcccaacag tccaagccagg 1620

tacgacagaa gtctgtctgg aaccaactcc gcgcagccta cgagaacgcc gggcccaaag 1680

tccagagccc ggccaacgtg ctcgagatcg agtggtcgaa gcagcagtat ttccaaggag 1740

ctccgagcgc cgtctatggg ctgaactgtc tcaacacact gggttcggcg ctcagaacgc 1800

cgttcaaggg tgttcatttc gttggaacgg agacgtcttt ggtttggaaa gggtatatgg 1860

aaggtgccat acgatcgggt cagcgaggcg ctgcagaagt tgtggctagc ctggtgccag 1920

cagcatag 1928

<210> 44
<211> 591
<212> PRT
<213> Rhinocladiella atrovirens

<400> 44

Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Leu Ala Ser Pro
1 5 10 15

Ala Gly Tyr Ser Tyr Val Gly Val Gly Pro Asn Gly Gly Arg Tyr Val
20 25 30

Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Ala Val Thr Asp Pro
35 40 45

Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
50 55 60

Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Ile Thr Lys Leu Asn Tyr
65 70 75 80

Tyr Ile Val Asp Tyr Asn Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
85 90 95

Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
100 105 110

Pro Val Pro Ala Leu Ala Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
115 120 125

Thr Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val
130 135 140

Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
145 150 155 160

Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
165 170 175

Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Gly Arg Thr Thr Ile Asn
180 185 190

Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Lys
195 200 205

Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly
210 215 220

Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr
225 230 235 240

Gly Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu
245 250 255

Pro Ala Ser Gln Leu Ile Glu Glu His Ser Leu Glu Asp Pro Lys Ala
260 265 270

Ser Pro Gln Ala Lys Gln Leu Asp Ser Val Ser Phe Ala His Tyr Cys
275 280 285

Glu Lys Leu Asn Leu Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg
290 295 300

Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Phe Phe Leu Thr
305 310 315 320

Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Val Ser Asp Lys

325 330 335

Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Leu
340 345 350

Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn
355 360 365

Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg
370 375 380

Ser Ala Ser Gly Gly Val Phe Arg Ser Lys Lys Val Val Leu Pro Thr
385 390 395 400

Leu Tyr Pro Thr Leu Ile Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
405 410 415

Ala Leu Ala Glu Lys Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
420 425 430

Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
435 440 445

Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Glu
450 455 460

Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
465 470 475 480

Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
485 490 495

Asn Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
500 505 510

Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
515 520 525

Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Cys Leu Asn Thr Leu Gly
530 535 540

Ser Ala Leu Arg Thr Pro Phe Lys Gly Val His Phe Val Gly Thr Glu
545 550 555 560

Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
565 570 575

Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
580 585 590

<210> 45
<211> 1928
<212> DNA
<213> Rhinocladiella atrovirens

<220>
<221> Intron
<222> (739)..(811)
<223>

<220>
<221> Intron
<222> (1134)..(1185)
<223>

<400> 45
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cacgtcggcg taggcccaaa cggagggagg tatgtgacaa tagctggaca gattggacaa 120

gacgcttcgg ccgtgacaga ccctgcctac gagaaacagg ttgcccaagc attcgccaac 180

ctgcgagctt gtcttgctgc agttggagcc acttcaaacg acattaccaa gctcaattac 240

tacatcgtcg actacaaccc gagcaaactc accgcaattg gagatgggct gaaggctacc 300

tttgcccttg acaggctccc tccttgcacg ctggtgccag tgccgggccc ggcttcacct 360

gaatacctct ttgaggttga tgctacggcg ctggttccag gacactcaac cccagacaat 420

gttgcggacg tggtcgtggt gggcgctggc ttgagcggtt tggagacggc acgcaaagtc 480

caggctgccg ggctgtcctg cctcgttctt gaggcgatgg atcgtgtggg gggaaagact 540

ctgagcgtac aatcgggtcc cggcaggacg actatcaatg acctcggcgc tgcgtggatc 600

aatgacagca accaaagcga agtattcaaa ttatttgaaa gatttcattt ggagggcgag 660

ctccagagga cgaccggaaa ttcaatccat caagcacaag acggtacaac cactacagct 720

ccttatggtg attccctggt aggcacaatt ccatcttgtg atgagacctc tgtcgtgtgt 780

agaatacagt cgctgactcc acatcgtcca gctgagcgag gaggttgcaa gtgcactcgc 840

ggaactcctt cccgcatggt ctcagctgat cgaagagcat agtcttgaag accccaaggc 900

gagccctcaa gcgaagcagc tcgacagtgt gagcttcgca cactactgtg agaaggatct 960

aaacttgcct gctgttctcg gcgtggcaaa ccagatcaca cgcgctctgc tcggtgtgga 1020

agcccacgag atcagcatgc ttttttctac cgactacatc aagagtgcca ccggtctcag 1080

taatattgtc tcggataaga aagacggtgg gcagtatatg cgatgcaaaa caggtgcgtg 1140

tggtgttctc tcagtgggag actcgttttt tagtggtcat tccaggtatg cagtcgcttt 1200

gccatgccat gtcaaaggaa cttgttccag gctcagtgca cctcaacacc ccggtcgccg 1260

aaattgagca gtcggcatcc ggctgtacag tacgatcggc ctcgggcggc gtgttccgaa 1320

gtaaaaaggt ggtggtttcg ttaccgacaa ccttgtatcc cacccttgata ttttcaccac 1380

ctcttccggc cgagaagcaa gcattggctg aaaaatccat cctgggctac tatagcaaga 1440

tagtcttcgt atgggacaag ctgtggtggc gcgaacaagg cttctcgggc gtcctccaat 1500

cgagctgtga ccccatctca tttgccagag ataccagcat cgaagtcgat cggcaatggt 1560

ccattacctg ttcatggtcc ggagaccggg gacggaagtg gtccgaacag tccaagccagg 1620

tacgacagaa gtctgtctgg aaccaacttc gcgcagccta cgagaacgcc ggggcccaag 1680

tccagagccc ggccaacgtg ctcgagatcg agtggtcgaa gcagcagtat ttccaaggag 1740

cgccgagcgc cgtctatggg ctgaactgtc tcaacacact gggttcggcg ctcagaacgc 1800

cgttcaaggg tgttcatttc gttggaacgg agacgtcttt ggtttggaaa gggtatatgg 1860

aaggggccat acgatcgggt cagcgaggcg ctgcagaagt tgtgcctagc ctggtgccag 1920

cagcatag 1928

<210> 46
<211> 591
<212> PRT
<213> Rhinocladiella atrovirens

<400> 46

Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Ala Ser Pro Ala
1 5 10 15

Gly Tyr Ser His Val Gly Val Gly Pro Asn Gly Gly Arg Tyr Val Thr
20 25 30

Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Ala Val Thr Asp Pro Ala
35 40 45

Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys Leu
50 55 60

Ala Ala Val Gly Ala Thr Ser Asn Asp Ile Thr Lys Leu Asn Tyr Tyr
65 70 75 80

Ile Val Asp Tyr Asn Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly Leu
85 90 95

Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val Pro
100 105 110

Val Pro Ala Leu Ala Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala Thr
115 120 125

Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val Val
130 135 140

Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln
145 150 155 160

Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly
165 170 175

Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn
180 185 190

Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Phe
195 200 205

Lys Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr
210 215 220

Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro
225 230 235 240

Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu
245 250 255

Leu Leu Pro Ala Trp Ser Gln Leu Ile Glu Glu His Ser Leu Glu Asp
260 265 270

Pro Lys Ala Ser Pro Gln Ala Lys Gln Leu Asp Ser Val Ser Phe Ala
275 280 285

His Tyr Cys Glu Lys Asp Leu Asn Leu Pro Ala Val Leu Gly Val Ala
290 295 300

Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser
305 310 315 320

Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn
325 330 335

Ile Val Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr
340 345 350

Gly Met Gln Ser Leu Cys His Ala Met Ser Lys Glu Leu Val Pro Gly
355 360 365

Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser
370 375 380

Gly Cys Thr Val Arg Ser Ala Ser Gly Gly Val Phe Arg Ser Lys Lys
385 390 395 400

Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Ile Phe Ser Pro Leu
405 410 415

Pro Ala Glu Lys Gln Ala Leu Ala Glu Lys Ser Ile Gly Tyr Tyr Ser
420 425 430

Lys Ile Val Phe Val Asp Lys Leu Trp Trp Arg Glu Gln Gly Phe Ser
435 440 445

Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr
450 455 460

Ser Ile Glu Val Asp Arg Gln Ser Ile Thr Cys Phe Met Val Gly Asp
465 470 475 480

Pro Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val
485 490 495

Trp Asn Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro
500 505 510

Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe
515 520 525

Gln Ala Pro Ser Ala Val Tyr Gly Leu Asn Cys Leu Asn Thr Leu Gly
530 535 540

Ser Ala Leu Arg Thr Pro Phe Lys Gly Val His Phe Val Gly Thr Glu
545 550 555 560

Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
565 570 575

Gln Arg Gly Ala Ala Glu Val Val Pro Ser Leu Val Pro Ala Ala
580 585 590

<210> 47
<211> 600
<212> PRT
<213> Exophiala spinifera

<400> 47

Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro
1 5 10 15

Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val
20 25 30

Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro
35 40 45

Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
50 55 60

Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr
65 70 75 80

Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
85 90 95

Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
100 105 110

Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
115 120 125

Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val
130 135 140

Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
145 150 155 160

Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
165 170 175

Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile
180 185 190

Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val
195 200 205

Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr
210 215 220

Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala
225 230 235 240

Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala
245 250 255

Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln
260 265 270

Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe
275 280 285

Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val
290 295 300

Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile
305 310 315 320

Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser
325 330 335

Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys
340 345 350

Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro
355 360 365

Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala
370 375 380

Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys
385 390 395 400

Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe
405 410 415

Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile
420 425 430

Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp
435 440 445

Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile
450 455 460

Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile
465 470 475 480

Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser
485 490 495

Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr
500 505 510

Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile
515 520 525

Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr
530 535 540

Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe
545 550 555 560

Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly
565 570 575

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Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val
            580                 585                 590

Val Ala Ser Leu Val Pro Ala Ala
        595                 600


<210>  48
<211>  1392
<212>  DNA
<213>  Unknown

<220>
<223>  Cys (-) APAO; removal of cys 461 (Exophiala spinifera)

<220>
<221>  CDS
<222>  (1)..(1392)
<223>

<400>  48
aaa gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt      48
Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
1               5                   10                  15

ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt      96
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val
            20                  25                  30

ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg     144
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
        35                  40                  45

ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat     192
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
    50                  55                  60

gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg     240
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
65                  70                  75                  80

gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa     288
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
                85                  90                  95

gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag     336
Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
            100                 105                 110

gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg     384
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu
        115                 120                 125

atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag     432
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
    130                 135                 140
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cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac      480
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
145                 150                 155                 160

ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctt      528
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu
                165                 170                 175

ggt gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc      576
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile
            180                 185                 190

aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc      624
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly
        195                 200                 205

ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc      672
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala
    210                 215                 220

atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc      720
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val
225                 230                 235                 240

gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg      768
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser
                245                 250                 255

ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc      816
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr
            260                 265                 270

ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa      864
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
        275                 280                 285

gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc      912
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
    290                 295                 300

gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc      960
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
305                 310                 315                 320

caa tcg agc tcc gac ccc atc tca ttt gcc aga gat acc agc atc gac     1008
Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
                325                 330                 335

gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga     1056
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
            340                 345                 350

cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg     1104
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
        355                 360                 365
```

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gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag      1152
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
     370                 375                 380

ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa      1200
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
385                 390                 395                 400

gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt      1248
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
                405                 410                 415

tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag      1296
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
            420                 425                 430

acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt      1344
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
        435                 440                 445

caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag      1392
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
    450                 455                 460
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<210> 49
<211> 463
<212> PRT
<213> Unknown

<220>
<223> Cys (-) APAO; removal of cysteine 461 (Exophiala spinifera)

<400> 49

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Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
1               5                   10                  15

Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val
            20                  25                  30

Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
        35                  40                  45

Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
    50                  55                  60

Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
65                  70                  75                  80

Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
                85                  90                  95
```

Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
100 105 110

Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu
115 120 125

Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
130 135 140

Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
145 150 155 160

Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu
165 170 175

Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile
180 185 190

Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly
195 200 205

Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala
210 215 220

Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val
225 230 235 240

Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser
245 250 255

Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr
260 265 270

Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
275 280 285

Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
290 295 300

Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
305 310 315 320

```
Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
                325                 330                 335

Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
            340                 345                 350

Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
        355                 360                 365

Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
    370                 375                 380

Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
385                 390                 395                 400

Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
                405                 410                 415

Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
            420                 425                 430

Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
        435                 440                 445

Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
    450                 455                 460
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<210> 50
<211> 1392
<212> DNA
<213> Unknown

<220>
<223> Cys (-) APA0; removal of cys 359 and 461 (Exophiala spinifera)

<220>
<221> CDS
<222> (1)..(1392)
<223>

<400> 50

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aaa gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt       48
Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
1               5                   10                  15

ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt       96
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val
```

```
                20                  25                  30

ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg      144
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
        35                  40                  45

ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat      192
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
    50                  55                  60

gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg      240
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
65                  70                  75                  80

gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa      288
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
                85                  90                  95

gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag      336
Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
            100                 105                 110

gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg      384
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu
        115                 120                 125

atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag      432
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
    130                 135                 140

cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac      480
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
145                 150                 155                 160

ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc      528
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu
                165                 170                 175

ggt gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc      576
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile
            180                 185                 190

aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc      624
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly
        195                 200                 205

ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tcg cat gcc      672
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala
    210                 215                 220

atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc      720
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val
225                 230                 235                 240

gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg      768
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser
                245                 250                 255
```

```
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc      916
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr
            260                 265                 270

ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa      964
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
        275                 280                 285

gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc     1012
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
    290                 295                 300

gta tgg gac aag ccg tgg tgg cgc gaa cag ggc ttc tcg ggc gtc ctc     1060
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
305                 310                 315                 320

caa tcg agc tcc gac ccc atc tca ttt gcc aga gat acc agc atc gac     1108
Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
                325                 330                 335

gtc atg cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga     1156
Val Met Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
            340                 345                 350

cgg aag tgg tcc caa cag tcc aag cag gta aga caa aag tct gtc tgg     1204
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
        355                 360                 365

gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag     1252
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
    370                 375                 380

ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa     1300
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
385                 390                 395                 400

gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt     1348
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
                405                 410                 415

tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag     1396
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
            420                 425                 430

acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt     1444
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
        435                 440                 445

caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag     1492
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
    450                 455                 460
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<210> 51
<211> 463
<212> PRT

<213> Unknown

<220>
<223> Cys (-) APAO; removal of cys 359 and 461 (Exophiala spinifera)

<400> 51

Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
1 5 10 15

Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val
20 25 30

Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
35 40 45

Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
50 55 60

Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
65 70 75 80

Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
85 90 95

Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
100 105 110

Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu
115 120 125

Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
130 135 140

Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
145 150 155 160

Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu
165 170 175

Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile
180 185 190

Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly
195 200 205

Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala
210 215 220

Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val
225 230 235 240

Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser
245 250 255

Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr
260 265 270

Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
275 280 285

Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
290 295 300

Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
305 310 315 320

Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
325 330 335

Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
340 345 350

Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
355 360 365

Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
370 375 380

Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
385 390 395 400

Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
405 410 415

Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
420 425 430

```
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
        435                 440                 445

Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
    450                 455                 460


<210>  52
<211>  1392
<212>  DNA
<213>  Unknown

<220>
<223>  Cys (-) APAO; removal of cys 169, 359, and 461 (Exophiala spinifera)

<220>
<221>  CDS
<222>  (1)..(1392)
<223>

<400>  52
aaa gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt       48
Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
1               5                   10                  15

ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg agc tcc ctc gtt       96
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Ser Leu Val
            20                  25                  30

ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg      144
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
        35                  40                  45

ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat      192
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
    50                  55                  60

gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg      240
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
65                  70                  75                  80

gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa      288
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
                85                  90                  95

gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag      336
Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
            100                 105                 110

gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg      384
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu
        115                 120                 125

atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag      432
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
```

```
    130                 135                 140

cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac      480
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
145                 150                 155                 160

ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc      528
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu
                165                 170                 175

ggt gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc      576
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile
            180                 185                 190

aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc      624
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly
        195                 200                 205

ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tcg cat gcc      672
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala
    210                 215                 220

atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc      720
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val
225                 230                 235                 240

gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg      768
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser
                245                 250                 255

ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc      816
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr
            260                 265                 270

ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa      864
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
        275                 280                 285

gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc      912
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
    290                 295                 300

gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc      960
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
305                 310                 315                 320

caa tcg agc tcc gac ccc atc tca ttt gcc aga gat acc agc atc gac     1008
Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
                325                 330                 335

gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga     1056
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
            340                 345                 350

cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg     1104
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
        355                 360                 365
```

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gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag      1152
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
     370                 375                 380

ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa      1200
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
385                 390                 395                 400

ggg gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt      1248
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
                405                 410                 415

tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag      1296
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
            420                 425                 430

acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt      1344
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
        435                 440                 445

caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag      1392
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
    450                 455                 460
```

<210> 53
<211> 463
<212> PRT
<213> Unknown

<220>
<223> Cys (-) APA0; removal of cys 169, 359, and 461 (Exophiala spinifera)

<400> 53

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Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
1               5                   10                  15

Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Ser Leu Val
            20                  25                  30

Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
        35                  40                  45

Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
    50                  55                  60

Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
65                  70                  75                  80

Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
```

85 90 95

Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
100 105 110

Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu
115 120 125

Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
130 135 140

Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
145 150 155 160

Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu
165 170 175

Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile
180 185 190

Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly
195 200 205

Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala
210 215 220

Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val
225 230 235 240

Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser
245 250 255

Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr
260 265 270

Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
275 280 285

Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
290 295 300

Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
305 310 315 320

Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
325 330 335

Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
340 345 350

Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
355 360 365

Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
370 375 380

Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
385 390 395 400

Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
405 410 415

Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
420 425 430

Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
435 440 445

Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
450 455 460